

TRANSMITTAL LETTER TO THE UNITED STATES  
DESIGNATED/ELECTED OFFICE (DO/EO/US)  
CONCERNING A FILING UNDER 35 U.S.C. 371

Attorney's Docket Number

05394.0011

U.S. Application No. 097673476

International Application. No.	International Filing Date	Priority Date Claimed
PCT/IB99/00740	April 16, 1999	April 16, 1998

## Title of Invention:

A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA LIBRARY. APPLICATION TO THE DETECTION OF MYCOBACTERIA

## Applicant(s) For DO/EO/US:

Stewart COLE, Roland BUCHRIESER-BROSCH, Stephen GORDON and Alain BILLAULT

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. [X] This is a FIRST submission of items concerning a filing under 35 U.S.C. 371.
2. [ ] This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371.
3. [ ] This express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).
4. [X] A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5. [X] A copy of the International Application as filed (35 U.S.C. 371(c)(2))
  - a. [X] is transmitted herewith (required only if not transmitted by the International Bureau).
  - b. [X] has been transmitted by the International Bureau.
  - c. [ ] is not required, as the application was filed in the United States Receiving Office (RO/US).
6. [ ] A translation of the International Application into English (35 U.S.C. 371(c)(2)).
7. [X] Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3)).
  - a. [ ] are transmitted herewith (required only if not transmitted by the International Bureau).
  - b. [ ] have been transmitted by the International Bureau.
  - c. [ ] have not been made; however, the time limit for making such amendments has NOT expired.
  - d. [X] have not been made and will not be made.
8. [ ] A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
9. [ ] An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).
10. [X] Annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).

## Items 11. to 16. below concern other document(s) or information included:

11. [ ] An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
12. [ ] An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
13. [ ] A FIRST preliminary amendment.
14. [ ] A SECOND or SUBSEQUENT preliminary amendment.
15. [ ] A substitute specification.
16. [X] A change of power of attorney and/or address letter.
- Other items or information:
  - a. [ ] Verified Small Entity Statement.
  - b. [ ] Copy of Notification of Missing Requirements.
  - c. [X] Copy of Cover Page of WIPO Publication (1 sheet).
  - d. [X] Sequence Listing (11 pages).

09/673476

17. [X] The following fees are submitted:

CALCULATIONS

Basic National Fee (37 CFR 1.492(a)(1)-(5)):

Search Report has been prepared by the EPO or JPO.....\$860.00

International preliminary examination fee paid to  
USPTO (37 CFR 1.482).....\$690.00No international preliminary examination fee paid to  
USPTO (37 CFR 1.482) but international search fee  
paid to USPTO (37 CFR 1.445(a)(2)).....\$760.00Neither international preliminary examination fee  
(37 CFR 1.482) nor international search fee  
(37 CFR 1.445(a)(2)) paid to USPTO.....\$1,000.00International preliminary examination fee paid to USPTO  
(37 CFR 1.482) and all claims satisfied provisions  
of PCT Article 33(1)-(4).....\$100.00

ENTER APPROPRIATE BASIC FEE AMOUNT =

\$ 860.00

Surcharge of \$130.00 for furnishing the oath or declaration later than

[ ] 20 [ ] 30 months from the earliest claimed priority date

(37 CFR 1.492(e)).

\$

Claims	Number Filed	Number Extra	Rate	
Total Claims	55 -20=	35	X \$18.00	\$ 630.00
Independent Claims	4 - 3=	1	X \$80.00	\$ 80.00
Multiple dependent claim(s) (if applicable)			+ \$270.00	\$ 270.00

TOTAL OF ABOVE CALCULATIONS =

\$1,840.00

Reduction by 1/2 for filing by small entity, if applicable. Verified

Small Entity statement must also be filed. (Note 37 CFR 1.9, 1.27, 1.28)

\$

SUBTOTAL =

\$1,840.00

Processing fee of \$130.00 for furnishing the English translation later  
than [ ] 20 [ ] 30 months from the earliest claimed priority date

\$

(37 CFR 1.492(f)).

+

TOTAL NATIONAL FEE =

\$1,840.00

Fee for recording the enclosed assignment (37 CFR 1.21(h)). The  
assignment must be accompanied by an appropriate cover sheet

(37 CFR 3.28, 3.31).

\$40.00 per property +

\$

TOTAL FEES ENCLOSED =

\$1,840.00

Amount to be

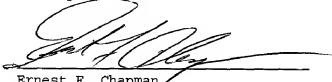
refunded \$

charged \$

- a. [X] A check in the amount of \$1,840.00 to cover the above fees is enclosed.
- b. [ ] Please charge my Deposit Account No. \_\_\_\_\_ in the amount of  
\$ \_\_\_\_\_ to cover the above fees. A duplicate copy of this sheet is  
enclosed.
- c. [X] The Commissioner is hereby authorized to charge any additional fees  
which may be required, or credit any overpayment to Deposit Account  
No. 06-0916. A duplicate copy of this sheet is enclosed.

The Commissioner is hereby authorized to charge any other fees due under 37 C.F.R. \$1.16  
or \$1.17 during the pendency of this application to our Deposit Account No. 06-0916.

SEND ALL CORRESPONDENCE TO:  
Finnegan, Henderson, Farabow  
Garrett & Dunner, L.L.P.  
1300 I Street, N.W.  
Washington, D.C. 20005-3315  
EFC/FPD/rgm

  
Ernest F. Chapman  
Reg. No. 25,961

Submitted: October 16, 2000

9/PRTS

1

A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST  
FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-  
BASED DNA LIBRARY APPLICATION TO THE DETECTION OF  
MYCOBACTERIA.

**I. Background of the invention**

The present invention pertains to a method for isolating a polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and that is absent or altered in the genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone belonging to a genomic DNA library of a given mycobacterium strain, said DNA library being cloned in a bacterial artificial chromosome (BAC). The invention concerns also polynucleotides identified by the above method, as well as detection methods for mycobacteria, particularly *Mycobacterium tuberculosis*, and kits using said polynucleotides as primers or probes. Finally, the invention deals with BAC-based mycobacterium DNA libraries used in the method according to the invention and particularly BAC-based *Mycobacterium tuberculosis* and *Mycobacterium bovis* BCG DNA libraries.

Radical measures are required to prevent the grim predictions of the World Health Organisation for the evolution of the global tuberculosis epidemic in the next century becoming a tragic reality. The powerful combination of genomics and bioinformatics is providing a wealth of information about the etiologic agent, *Mycobacterium tuberculosis*, that will facilitate the conception and development of new therapies. The start point for genome sequencing was the integrated map of the 4.4 Mb circular chromosome of the widely-used, virulent reference strain, *M. tuberculosis* H37Rv and appropriate cosmids were subjected to systematic shotgun sequence analysis at the Sanger Centre.

Cosmid clones (Balasubramanian et al., 1996; Pavelka et al., 1996) have played a crucial role in the *M. tuberculosis* H37Rv genome sequencing project. However, problems such as under-representation of certain regions of the chromosome, unstable inserts and the relatively small insert size complicated the production of a comprehensive set of canonical cosmids representing the entire genome.

## II. Summary of the invention

In order to avoid the numerous technical constraints encountered in the state of the art, as described hereabove, when using genomic mycobacterial DNA libraries constructed in cosmid clones, the inventors have attempted to realize genomic mycobacterial DNA libraries in an alternative type of vectors, namely Bacterial Artificial Chromosome (BAC) vectors.

The success of this approach depended on whether the resulting BAC clones could maintain large mycobacterial DNA inserts. There are various reports describing the successful construction of a BAC library for eucaryotic organisms (Cai et al., 1995; Kim et al., 1996; Misumi et al., 1997; Woo et al., 1994; Zimmer et al., 1997) where inserts up to 725 kb (Zimmer et al., 1997) were cloned and stably maintained in the *E. coli* host strain.

Here, it is shown that, surprisingly, the BAC system can also be used for mycobacterial DNA, as 70% of the clones contained inserts in the size of 25 to 104 kb.

This is the first time that bacterial, and specifically mycobacterial, DNA is cloned in such BAC vectors.

In an attempt to obtain complete coverage of the genome with a minimal overlapping set of clones, a Bacterial Artificial Chromosome (BAC) library of *M. tuberculosis* was constructed, using the vector pBeloBAC11 (Kim et al., 1996) which combines a simple phenotypic screen for recombinant clones with the stable propagation of large inserts (Shizuya et al., 1992). The BAC cloning system is based on the *E. coli* F-factor, whose replication is strictly controlled and thus ensures stable maintenance of large constructs (Willets et al., 1987). BACs have been widely used for cloning of DNA from various eucaryotic species (Cai et al., 1995; Kim et al., 1996; Misumi et al., 1997; Woo et al., 1994; Zimmer et al., 1997). In contrast, to our knowledge this report describes the first attempt to use the BAC system for cloning bacterial DNA.

A central advantage of the BAC cloning system over cosmid vectors used in prior art is that the F-plasmid is present in only one or a maximum of two copies per cell, reducing the potential for recombination between DNA fragments and, more importantly, avoiding the lethal overexpression of cloned bacterial genes. However, the presence of the BAC as just a single copy means that plasmid DNA has to be extracted from a large volume of culture to obtain

sufficient DNA for sequencing and it is described here in the examples a simplified protocol to achieve this.

Further, the stability and fidelity of maintenance of the clones in the BAC library represent ideal characteristics for the identification of genomic differences possibly responsible for phenotypic variations in different mycobacterial species.

As it will be shown herein, BACs can be allied with conventional hybridization techniques for refined analyses of genomes and transcriptional activity from different mycobacterial species.

Having established a reliable procedure to screen for genomic polymorphisms, it is now possible to conduct these comparisons on a more systematic basis than in prior art using representative BACs throughout the chromosome and genomic DNA from a variety of mycobacterial species.

As another approach to display genomic polymorphisms, the inventors have also started to use selected H37Rv BACs for "molecular combing" experiments in combination with fluorescent *in situ* hybridization (Bensimon et al., 1994; Michalet et al., 1997). With such techniques the one skilled in the art is enabled to explore the genome of mycobacteria in general and of *M. tuberculosis* in particular for further polymorphic regions.

The availability of BAC-based genomic mycobacterial DNA libraries constructed by the inventors have allowed them to design methods and means both useful to identify genomic regions of interest of pathogenic mycobacteria, such as *Mycobacterium tuberculosis*, that have no counterpart in the corresponding non-pathogenic strains, such as *Mycobacterium bovis* BCG, and useful to detect the presence of polynucleotides belonging to a specific mycobacterium strain in a biological sample.

By a biological sample according to the present invention, it is notably intended a biological fluid, such as plasma, blood, urine or saliva, or a tissue, such as a biopsy.

Thus, a first object of the invention consists of a method for isolating a polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and that is absent or altered in the genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone belonging to a genomic DNA library of a given mycobacterium strain, said DNA library being cloned in a bacterial artificial chromosome (BAC).

The invention is also directed to a polynucleotide of interest that has been isolated according to the above method and in partoualar a polynucleotide containing one or several Open Reading Frames (ORFs), for example ORFs encoding either a polypeptide involved in the pathogenicity of a mycobacterium strain or ORFs encoding Polymorphic Glycine Rich Sequences (PGRS).

Such polynucleotides of interest may serve as probes or primers in order to detect the presence of a specific mycobacterium strain in a biological sample or to detect the expression of specific genes in a particular mycobacterial strain of interest.

The BAC-based genomic mycobacterial DNA libraries generated by the present inventors are also part of the invention, as well as each of the recombinant BAC clones and the DNA insert contained in each of said recombinant BAC clones.

The invention also pertains to methods and kits for detecting a specific mycobacterium in a biological sample using either at least one recombinant BAC clone or at least one polynucleotide according to the invention, as well as to methods and kits to detect the expression of one or several specific genes of a given mycobacterial strain present in a biological sample.

### III. Brief description of the Figures.

In order to better understand the present invention, reference will be made to the appended figures which depicted specific embodiments to which the present invention is in no case limited in scope with.

**Figures 1A and 1B :** PCR-screening for unique BAC clones with specific primers for 2 selected genomic regions of the H37Rv chromosome, using 21 pools representating 2016 BACs (Figure 1A) and sets of 20 subpools from selected positive pools (Figure 1B).

**Figure 2 :** Pulsed-field gel electrophoresis gel of *DraI*- cleaved BAC clones used for estimating the insert sizes of BACs.

**Figure 3 :** Minimal overlapping BAC map of *M. tuberculosis* H37Rv superimposed on the integrated physical and genetic map established by Philipp et al. (18). Y- and I- numbers show pYUB328 (2) and pYUB412 (16) cosmids which were shotgun sequenced during the H37Rv genome sequencing project. Y-cosmids marked with \* were shown in the integrated physical and genetic map

(18). Rv numbers show the position of representative BAC clones relative to sequenced Y- and I- clones. Squared Rv numbers show BACs which were shotgun sequenced at the Sanger Centre.

**Figures 4A and 4B :** Ethidium bromide stained gel (Figure 4A) and corresponding Southern blot (Figure 4B) of *Eco*RI and *Pvu*II digested Rv58 DNA hybridized with <sup>32</sup>P labeled genomic DNA preparations from *M. tuberculosis* H37Rv, *M. bovis* ATCC 19210 and *M. bovis* BCG Pasteur.

**Figure 5 :** Organisation of the ORFs in the 12.7 kb genomic region present in *M. tuberculosis* H37Rv but not present in *M. bovis* ATCC 19210 and *M. bovis* BCG Pasteur. Arrows show the direction of transcription of the putative genes. Positions of *Eco*RI and *Pvu*II restriction sites are shown. Vertical dashes represent stop codons. The 11 ORFs correspond to the ORFs MTCY277.28 to MTCY277.38 / accession number Z79701 -EMBL Nucleotide Sequence Data Library. The junction sequences flanking the polymorphic region are shown.

**Figure 6 :** Variation in the C-terminal part of a PE-PGRS open reading frame in *M. tuberculosis* strain H37Rv relative to *M. bovis* BCG strain Pasteur.

The numbers on the right side of the Figure denote the position of the end nucleotides, taking as the reference the *M. tuberculosis* genome.

**Figure 7 :** Polynucleotide sequence next to the *Hind*III cloning site in the BAC vector pBeloBAC11 (Kim et al., 1996) used to clone the inserts of the BAC-based myobacterial genomic DNA library according to the invention.

NotI : location of the NotI restriction sites.

Primer T7-BAC1 : nucleotide region recognized by the T7-BAC1 primer shown in Table 1.

T7 promoter : location of the T7 promoter region on the pBeloBac11 vector.

Primer T7-Belo2 : nucleotide region recognized by the T7-Belo2 primer shown in Table 1.

*Hind* III : the *Hind*III cloning site used to clone the genomic inserts in the pBeloBAC11 vector.

SP6-Mid primer : nucleotide region recognized by the SP6 Mid primer shown in Table 1.

SP6-BAC1 primer : nucleotide region recognized by the SP6 BAC1 primer shown in Table 1.

SP6 promoter : location of the SP6 promoter region on the pBeloBac11 vector.

#### IV. Detailed description of the preferred embodiments.

As already mentioned hereinbefore, the present invention is directed to a method for isolating a polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and that is absent or altered in the genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone belonging to a genomic DNA library of a given mycobacterium strain, said DNA library being cloned in a bacterial artificial chromosome (BAC) type vector.

For this purpose, the inventors have constructed several BAC-based mycobacterial genomic DNA libraries that may be used in order to perform the above described method.

Because it is the first time that mycobacterial genomic DNA has been successfully cloned in BAC type vectors, and because these DNA libraries are then novel and nonobvious, an object of the present invention consists in a mycobacterial genomic DNA library cloned in such a BAC type vector.

As an illustrative example, a BAC-based DNA library of *Mycobacterium tuberculosis* has been realized. Forty-seven cosmids chosen from the integrated map of the 4.4 Mb circular chromosome (Philipp et al., 1996a) were shotgun-sequenced during the initial phase of the H37Rv genome sequence project. The sequences of these clones were used as landmarks in the construction of a minimally overlapping BAC map. Comparison of the sequence data from the termini of 420 BAC clones allowed us to establish a minimal overlapping BAC map and to fill in the existing gaps between the sequence of cosmids. As well as using the BAC library for genomic mapping and sequencing, we also tested the system in comparative genomic experiments in order to uncover differences between two closely related mycobacterial species. As shown in a previous study (Philipp et al., 1996b), *M. tuberculosis*, *M. bovis* and *M. bovis* BCG, specifically BCG Pasteur strain, exhibit a high level of global genomic conservation, but certain polymorphic regions were also detected. Therefore, it was of great interest to find a reliable, easy and rapid way to exactly localize polymorphic regions in mycobacterial genomes using selected BAC clones. This approach was validated by determining the exact size and location of the polymorphisms in the genomic region of *DraI* fragment Z4 (Philipp et al., 1996b), taking advantage of the availability of an appropriate BAC clone covering the polymorphic region and



the H37Rv genome sequence data. This region is located approximately 1.7 Mb from the origin of replication.

The Bacterial Artificial Chromosome (BAC) cloning system is capable of stably propagating large, complex DNA inserts in *Escherichia coli*. As part of the *Mycobacterium tuberculosis* H37Rv genome sequencing project, a BAC library was constructed in the pBeloBAC11 vector and used for genome mapping, confirmation of sequence assembly, and sequencing. The library contains about 5000 BAC clones, with inserts ranging in size from 25 to 104 kb, representing theoretically a 70 fold coverage of the *M. tuberculosis* genome (4.4 Mb). A total of 840 sequences from the T7 and SP6 termini of 420 BACs were determined and compared to those of a partial genomic database. These sequences showed excellent correlation between the estimated sizes and positions of the BAC clones and the sizes and positions of previously sequenced cosmids and the resulting contigs. Many BAC clones represent linking clones between sequenced cosmids, allowing full coverage of the H37Rv chromosome, and they are now being shotgun-sequenced in the framework of the H37Rv sequencing project. Also, no chimeric, deleted or rearranged BAC clones were detected, which was of major importance for the correct mapping and assembly of the H37Rv sequence. The minimal overlapping set contains 68 unique BAC clones and spans the whole H37Rv chromosome with the exception of a single gap of ~ 150 kb. As a post-genomic application, the canonical BAC set was used in a comparative study to reveal chromosomal polymorphisms between *M. tuberculosis*, *M. bovis* and *M. bovis* BCG Pasteur, and a novel 12.7 kb segment present in *M. tuberculosis* but absent from *M. bovis* and *M. bovis* BCG was characterized. This region contains a set of genes whose products show low similarity to proteins involved in polysaccharide biosynthesis. The H37Rv BAC library therefore provides the one skilled in the art with a powerful tool both for the generation and confirmation of sequence data as well as for comparative genomics and a plurality of post-genomic applications.

The above described BAC-based *Mycobacterium tuberculosis* genomic DNA library is part of the present invention and has been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on November 19, 1997 under the accession number I-1945.

Another BAC-based DNA library has been constructed with the genomic DNA of *Mycobacterium bovis* BCG, Pasteur strain, and said DNA library has

P 21.08.00

228 Res. PCT/PTO 16 OCT 2000

been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on June 30, 1998 under the accession number I-2049.

Thus, as a specific embodiment of the above described method for isolating a polynucleotide of interest said method makes use of at least one BAC-based DNA library that has been constructed from the genomic DNA of *Mycobacterium tuberculosis*, more specifically of the H37Rv strain and particularly of the DNA library deposited in the accession number I-1945.

In another specific embodiment of the above described method for isolating a polynucleotide of interest said method makes use of at least one BAC-based DNA library has been constructed from the genomic DNA of *Mycobacterium bovis* BCG, more specifically of the Pasteur strain and particularly of the DNA library deposited in the accession number I-2049.

In more details, the method according to the invention for isolating a polynucleotide of interest may comprise the following steps :

- a) isolating at least one polynucleotide contained in a clone of a BAC-based DNA library of mycobacterial origin;
- b) isolating :
  - at least one genomic or cDNA polynucleotide from a mycobacterium, said mycobacterium belonging to a strain different from the strain used to construct the BAC-based DNA library of step a); or alternatively
  - at least one polynucleotide contained in a clone of a BAC-based DNA library prepared from the genome of a mycobacterium that is different from the mycobacterium used to construct the BAC-based DNA library of step a);
- c) hybridizing the at least one polynucleotide of step a) to the at least one polynucleotide of step b);
- d) selecting the at least one polynucleotide of step a) that has not formed a hybrid complex with the at least one polynucleotide of step b);
- e) characterizing the selected polynucleotide.

Following the above procedure, the at least one polynucleotide of step a) may be prepared as follows :

- 1) digesting at least one recombinant BAC clone by an appropriate restriction endonuclease in order to isolate the polynucleotide insert of interest from the vector genetic material;
- 2) optionally amplifying the resulting polynucleotide insert;

3) optionally digesting the polynucleotide insert of step 1) or step 2) with at least one restriction endonuclease.

The above method of the invention allows the one skilled in the art to perform comparative genomics between different strains or species of mycobacteria cells, for example between pathogenic strains or species and their non pathogenic strains or species counterparts, as it is the illustrative case for the genomic comparison between *Mycobacterium tuberculosis* and *Mycobacterium bovis* BCG that is described herein in the examples.

Restriction digests of a given clone of a BAC library according to the invention may be blotted to membranes, and then probed with radiolabeled DNA form another strain or another species of mycobacteria, allowing the one skilled in the art to identify, characterize and isolate a polynucleotide of interest that may be involved in important metabolic and/or physiological pathways of the mycobacterium under testing, such as a polynucleotide functionally involved in the pathogenicity of said given mycobacteria for its host organism.

More specifically, the inventors have shown in Example 6 that when restriction digests of a given clone of the BAC library identified by the CNCM accession number I-1945 are blotted to membranes and then probed with radiolabeled total genomic DNA from, for example, *Mycobacterium bovis* BCG Pasteur, it is observed that restriction fragments that fail to hybridize with the *M. bovis* BCG Pasteur DNA are absent from its genome, hence identifying polymorphic regions between *M. bovis* BCG Pasteur and *M. tuberculosis* H37Rv.

Thus, a further object of the present invention consists in a polynucleotide of interest that has been isolated according to the method described herein before.

In Example 6, a polynucleotide of approximately 12.7 kilobases has been isolated that is present in the genome of *M. tuberculosis* but is absent of the genome of *M. bovis* BCG. This polynucleotide of interest contains 11 ORFs that may be involved in polysaccharide biosynthesis. In particular, two of said ORFs are of particular interest, namely ORF6 (MTCY277.33; Rv1511) that encodes a protein that shares significant homology with bacterial GDP-D-mannose dehydratases, whereas the protein encoded by ORF7 (MTCY277.34; Rv1512) shares significant homology with a nucleotide sugar epimerase. As polysaccharide is a major constituent of the mycobacterial cell wall, these deleted genes may cause the cell wall of *M. bovis* BCG to differ from that of *M. tuberculosis*, a fact that may have important consequences for both the immune

response to *M. bovis* BCG and virulence. Detection of such a polysaccharide is of diagnostic interest and possibly useful in the design of tuberculosis vaccines.

Consequently, the polynucleotide of interest obtained following the method according to the invention may contain at least one ORF, said ORF preferably encoding all or part of a polypeptide involved in an important  
5 metabolic and/or physiological pathway of the mycobacteria under testing, and more specifically all or part of a polypeptide that is involved in the pathogenicity of the mycobacteria under testing, such as for example *Mycobacterium tuberculosis*, and more generally mycobacteria belonging to the *Mycobacterium tuberculosis* complex.  
10

The *Mycobacterium tuberculosis* complex has its usual meaning, i.e. the complex of mycobacteria causing tuberculosis which are *Mycobacterium tuberculosis*, *Mycobacterium bovis*, *Mycobacterium africanum*, *Mycobacterium microi* and the vaccine strain *Mycobacterium bovis* BCG.

An illustrative polynucleotide of interest according to the present invention comprises all or part of the polynucleotide of approximately 12.7 kilobases that is present in the genome of *M. tuberculosis* but is absent from the genome of *M. bovis* BCG disclosed hereinbefore. This polynucleotide is contained in clone Rv58 of the BAC DNA library I-1945.  
15

Generally, the invention also pertains to a purified polynucleotide comprising the DNA insert contained in a recombinant BAC vector belonging to a BAC-based mycobacterial genomic DNA library, such as for example the I-1945 BAC DNA library.  
20

Advantageously, such a polynucleotide has been identified according to the method of the invention.  
25

Such a polynucleotide of interest may be used as a probe or a primer useful for specifically detecting a given mycobacterium of interest, such as *Mycobacterium tuberculosis* or *Mycobacterium bovis* BCG.

More specifically, the invention then deals with a purified polynucleotide useful as probe or a primer comprising all or part of the nucleotide sequence SEQ ID N°1.  
30

The location, on the *Mycobacterium tuberculosis* chromosome, of the above polynucleotide of sequence SEQ ID N°1 has now been ascribed to begin, at its 5' end at nucleotide at position nt 1696015 and to end, at its 3' end, at nucleotide at position nt 1708746.  
35

For diagnostic purposes, this 12.7 kb deletion should allow a rapid PCR screening of tubercle isolates to identify whether they are bovine or human strains. The primers listed in Table 1 are flanking the deleted region and give a 722 bp amplicon in *M. bovis* or *M. bovis* BCG strains, but a fragment of 13,453 bp in *M. tuberculosis* that is practically impossible to amplify under the same PCR conditions. More importantly, assuming that some of the gene products from this region represent proteins with antigenic properties, it could be possible to develop a test that can reliably distinguish between the immune response induced by vaccination with *M. bovis* BCG vaccine strains and infection with *M. tuberculosis* or that the products (e.g. polysaccharides) are specific immunogens.

The invention also provides for a purified polynucleotide useful as a probe or as a primer, said polynucleotide being chosen in the following group of polynucleotides :

- a) a polynucleotide comprising at least 8 consecutive nucleotides of the sequence SEQ ID N°1;
- b) a polynucleotide whose sequence is fully complementary to the sequence of the polynucleotide defined in a);
- c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).

For the purpose of defining a polynucleotide or oligonucleotide hybridizing under stringent hybridization conditions, such as above, it is intended a polynucleotide that hybridizes with a reference polynucleotide under the following hybridization conditions.

The hybridization step is realized at 65°C in the presence of 6 x SSC buffer, 5 x Denhardt's solution, 0.5% SDS and 100µg/ml of salmon sperm DNA.

For technical information, 1 x SSC corresponds to 0.15 M NaCl and 0.05M sodium citrate; 1 x Denhardt's solution corresponds to 0.02% Ficoll, 0.02% polyvinylpyrrolidone and 0.02% bovine serum albumin.

The hybridization step is followed by four washing steps :

- two washings during 5 min, preferably at 65°C in a 2 x SSC and 0.1%SDS buffer,
- one washing during 30 min, preferably at 65°C in a 2 x SSC and 0.1% SDS buffer,
- one washing during 10 min, preferably at 65°C in a 0.1 x SSC and 0.1%SDS buffer.

A first illustrative useful polynucleotide that is included in the polynucleotide of sequence SEQ ID N°1 is the polynucleotide of sequence SEQ ID N°2 that corresponds to the Sp6 end-sequence of SEQ ID N°1.

A second illustrative useful polynucleotide that is included in the polynucleotide of sequence SEQ ID N°1 is the polynucleotide of sequence SEQ ID N°3 that corresponds to the T7 end-sequence of SEQ ID N°1, located on the opposite strand.

The polynucleotide of sequence SEQ ID N°1 contains 11 ORFs, the respective locations of which, taking into account the orientation of each ORF on the chromosome, on the sequence of the *Mycobacterium tuberculosis* chromosome, is given hereafter :

- The location of ORF1 is comprised between nucleotide at position nt 1695944 and nucleotide at position nt1696441.
- The location of ORF2 is comprised between nucleotide at position nt 1696728 and nucleotide at position nt1697420.
- The location of ORF3 is comprised between nucleotide at position nt 1698096 and nucleotide at position nt1699892. ORF3 probably encodes a protein having the characteristics of a membrane protein.
- The location of ORF4 is comprised between nucleotide at position nt 1700210 and nucleotide at position nt1701088.
- The location of ORF5 is comprised between nucleotide at position nt 1701293 and nucleotide at position nt1702588. ORF5 encodes a protein having the characteristics of a membrane protein.
- The location of ORF6 is comprised between nucleotide at position nt 1703072 and nucleotide at position nt1704091. ORF6 encodes a protein having the characteristics of a GDP-D-mannose dehydratase.
- The location of ORF7 is comprised between nucleotide at position nt 1704091 and nucleotide at position nt1705056. ORF7 encodes a protein having the characteristics of a nucleotide sugar epimerase involved in colanic acid biosynthesis.
- The location of ORF8 is comprised between nucleotide at position nt 1705056 and nucleotide at position nt1705784.
- The location of ORF9 is comprised between nucleotide at position nt 1705808 and nucleotide at position nt1706593. ORF9 encodes a protein having the characteristics of colanic acid biosynthesis glycosyl transferase.

- The location of ORF10 is comprised between nucleotide at position nt 1706631 and nucleotide at position nt1707524.

- The location of ORF11 is comprised between nucleotide at position nt 1707530 and nucleotide at position nt1708648. ORF11 encodes a protein similar to a spore coat polysaccharide biosynthesis.

A polynucleotide of interest obtained by the above-disclosed method according to the invention may also contain at least one ORF that encodes all or part of acidic, glycine-rich proteins, belonging to the PE and PPE families, whose genes are often clustered and based on multiple copies of the polymorphic repetitive sequences. The names PE and PPE derive from the fact that the motifs ProGlu (PE, positions 8, 9) and ProProGlu (PPE, positions 7 to 9) are found near the N-terminus in almost all cases. The PE protein family all have a highly conserved N-terminal domain of ~110 amino acid residues, that is predicted to have a globular structure, followed by a C-terminal segment which varies in size, sequence and repeat copy number. Phylogenetic analysis separated the PE family into several groups, the larger of which is the highly repetitive PGRS class containing 55 members whereas the other groups share very limited sequence similarity in their C-terminal domains. The predicted molecular weights of the PE proteins vary considerably as a few members only contain the ~110 amino acid N-terminal domain while the majority have C-terminal extensions ranging in size from 100 up to >1400 residues. A striking feature of the PGRS proteins is their exceptional glycine content (up to 50%) due to the presence of multiple tandem repetitions of GlyGlyAla or GlyGlyAsn motifs or variations thereof.

Like the PE family, the PPE protein family also has a conserved N-terminal domain that comprises ~180 amino acid residues followed by C-terminal segments that vary considerably in sequence and length. These proteins fall into at least three groups, one of which constitutes the MPTR class characterised by the presence of multiple, tandem copies of the motif AsnXGlyXGlyAsnXGly. The second subgroup contains a characteristic, well-conserved motif around position 350 (GlyXXSerValProXXTrp), whereas the other group contains proteins that are unrelated except for the presence of the common 180-residue PPE domain. C-terminal extensions may range in size from 00 up to 3500 residues.

One member of the PGRS sub-family, the WHO antigen 22T (Abou-Zeid et al., 1991), a 55kD protein capable of binding fibronectin, is produced during

21.06.00

14

disease and elicits a variable antibody response suggesting either that individuals mount different immune responses or that this PGRS-protein may not be produced in this form by all strains of *M. tuberculosis*. In other words, at least some PE\_PGRS coding sequences encode for proteins that are involved in the recognition of *M. tuberculosis* by the immune system of the infected host. Therefore, differences in the PGRS sequences could represent the principal source of antigenic variation in the otherwise genetically and antigenically homogeneous bacterium.

By performing the method of the invention using the *M. tuberculosis* BAC based DNA library I-1945, the inventors have discovered the occurrence of sequence differences between a given PGRS encoding ORF (ORF reference on the genomic sequence of *M. tuberculosis* Rv0746) of *M. tuberculosis* and its counterpart sequence in the genome of *M. bovis* BCG.

More precisely, the inventors have determined that one ORF contained in BAC vector N° Rv418 of the *M. tuberculosis* BCG I-1945 DNA library carries both base additions and base deletions when compared with the corresponding ORF in the genome of *M. bovis* BCG that is contained in the BAC vector N° X0175 of the *M. bovis* BCG I-2049 DNA library. The variations observed in the base sequences correspond to variations in the C-terminal part of the amino acid sequence of the PGRS ORF translation product.

As shown in Figure 6, an amino acid stretch of 9 residues in length is present in this *M. tuberculosis* PGRS (ORF reference Rv0746) and is absent from the ORF counterpart of *M. bovis* BCG, namely the following amino acid sequence:

NH<sub>2</sub>-GGAGGAGGSSAGGGGAGGAGGAGGWLLGD-COOH.

Furthermore, Figure 6 shows also that an amino acid stretch of 45 residues in length is absent from this *M. tuberculosis* PGRS and is present in the ORF counterpart of *M. bovis* BCG, namely following amino acid sequence:

NH<sub>2</sub>-GAGGIGGIGGNANGGAGGNGGTGGQLWGS GGAGVEGGAAL

SVGDT-COOH.

Similar observations were made with PPE ORF Rv0442, which showed a 5 codon deletion relative to a *M. bovis* amino acid sequence.

Given that the polymorphism associated with the PE-PGRS or PEE ORFS resulted in extensive antigenic variability or reduced antigen presentation, this would be of immense significance for vaccine design, for understanding



M 21.06.00

protective immunity in tuberculosis and, possibly, explain the varied responses seen in different BCG vaccination programmes.

There are several striking parallels between the PGRS proteins and the Epstein-Barr virus-encoded nuclear antigens (EBNA). Both polypeptide families are glycine-rich, contain Gly-Ala repeats that represent more than one third of the molecule, and display variation in the length of the repeat region between different isolates. The Gly-Ala repeat region of EBNA1 has been shown to function as a *cis*-acting inhibitor of antigen processing and MHC class I-restricted antigen presentation (Levitskaya et al., 1995). The fact that MHC class I knock-out mice are extremely susceptible to *M. tuberculosis* underlines the importance of MHC class I antigen presentation in protection against tuberculosis. Therefore, it is possible that the PE/PPE protein family also play some role in inhibiting antigen presentation, allowing the bacillus to hide from the host's immune system.

As such the novel and nonobvious PGRS polynucleotide from *M. bovis* which is homolog to the *M. tuberculosis* ORF Rv0746, and which is contained in the BAC clone N° X0175 (See Table 4 for SP6 and T7 end-sequences of clone n° X0175) of the I-2049 *M. bovis* BCG BAC DNA library is part of the present invention, as it represents a starting material in order to define specific probes or primers useful for detection of antigenic variability in mycobacterial strains, possible inhibition of antigen processing as well as to differentiate *M. tuberculosis* from *M. bovis* BCG.

Thus, a further object of the invention consists in a polynucleotide comprising the sequence SEQ ID N°4.

Polynucleotides of interest have been defined by the inventors as useful detection tools in order to differentiate *M. tuberculosis* from *M. bovis* BCG. Such polynucleotides are contained in the 45 aminoacid length coding sequence that is present in *M. bovis* BCG but absent from *M. tuberculosis*. This polynucleotide has a sequence beginning (5'end) at the nucleotide at position nt 729 of the sequence SEQ ID N°4 and ending (3'end) at the nucleotide in position nt 863 of the sequence SEQ ID N°4.

Thus, part of the present invention is also a polynucleotide which is chosen among the following group of polynucleotides :

a) a polynucleotide comprising at least 8 consecutive nucleotides of the nucleotide sequence SEQ ID N°5 ;

b) a polynucleotide which sequence is fully complementary to the sequence of the polynucleotide defined in a) ;

c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).

5 The stringent hybridization conditions for the purpose of defining the above disclosed polynucleotide are defined herein before in the specification.

The invention also provides for a BAC-based *Mycobacterium tuberculosis* strain H37Rv genomic DNA library that has been deposited in the Collection Nationale de Cultures de Microorganismes on November 19, 1997 under the  
10 accession number I-1945.

A further object of the invention consists in a recombinant BAC vector which is chosen among the group consisting of the recombinant BAC vectors belonging to the BAC-based DNA library I-1945.

Generally, a recombinant BAC vector of interest may be chosen among  
15 the following set or group of BAC vectors contained in the BAC-based DNA library I-1945 :

Rv101; Rv102; Rv103; Rv104; Rv105; Rv106; Rv107; Rv108; Rv109; Rv10;  
Rv110; Rv111; Rv112; Rv113; Rv114; Rv115; Rv116; Rv117; Rv118; Rv119;  
Rv11; Rv120; Rv121; Rv122; Rv123; Rv124; Rv126; Rv127; Rv128; Rv129;  
20 Rv130; Rv132; Rv134; Rv135; Rv136; Rv137; Rv138; Rv139; Rv13; Rv140;  
Rv141; Rv142; Rv143; Rv144; Rv145; Rv146; Rv147; Rv148; Rv149; Rv14;  
Rv150; Rv151; Rv152; Rv153; Rv154; Rv155; Rv156; Rv157; Rv159; Rv15;  
Rv160; Rv161; Rv162; Rv163; Rv164; Rv165; Rv166; Rv167; Rv169; Rv16;  
Rv170; Rv171; Rv172; Rv173; Rv174; Rv175; Rv176; Rv177; Rv178; Rv179;  
25 Rv17; Rv180; Rv181; Rv182; Rv183; Rv184; Rv185; Rv186; Rv187; Rv188;  
Rv18; Rv190; Rv191; Rv192; Rv193; Rv194; Rv195; Rv196; Rv19; Rv1; Rv201;  
Rv204; Rv205; Rv207; Rv209; Rv20; Rv214; Rv215; Rv217; Rv218; Rv219;  
Rv21; Rv220; Rv221; Rv222; Rv223; Rv224; Rv225; Rv226; Rv227; Rv228;  
Rv229; Rv22; Rv230; Rv231; Rv232; Rv233; Rv234; Rv235; Rv237; Rv240;  
30 Rv241; Rv243; Rv244; Rv245; Rv246; Rv247; Rv249; Rv24; Rv251; Rv252;  
Rv253; Rv254; Rv255; Rv257; Rv258; Rv259; Rv25; Rv260; Rv261; Rv262;  
Rv263; Rv264; Rv265; Rv266; Rv267; Rv268; Rv269; Rv26; Rv270; Rv271;  
Rv272; Rv273; Rv274; Rv275; Rv276; Rv277; Rv278; Rv279; Rv27; Rv280;  
Rv281; Rv282; Rv283; Rv284; Rv285; Rv286; Rv287; Rv288; Rv289; Rv28;  
35 Rv290; Rv291; Rv292; Rv293; Rv294; Rv295; Rv296; Rv29; Rv2; Rv301;

Rv302; Rv303; Rv304; Rv306; Rv307; Rv308; Rv309; Rv30; Rv310; Rv311;  
 Rv312; Rv313; Rv314; Rv315; Rv316; Rv317; Rv318; Rv319; Rv31; Rv32;  
 Rv322; Rv327; Rv328; Rv329; Rv32; Rv330; Rv331; Rv333; Rv334; Rv335;  
 Rv336; Rv337; Rv338; Rv339; Rv33; Rv340; Rv341; Rv343; Rv344; Rv346;  
 5 Rv347; Rv348; Rv349; Rv34; Rv350; Rv351; Rv352; Rv353; Rv354; Rv355;  
 Rv356; Rv357; Rv358; Rv359; Rv35; Rv360; Rv361; Rv363; Rv364; Rv365;  
 Rv366; Rv367; Rv368; Rv369; Rv36; Rv370; Rv371; Rv373; Rv374; Rv375;  
 Rv376; Rv377; Rv378; Rv379; Rv37; Rv381; Rv382; Rv383; Rv384; Rv385;  
 Rv386; Rv387; Rv388; Rv389; Rv38; Rv390; Rv391; Rv392; Rv393; Rv396;  
 10 Rv39; Rv3; Rv40; Rv412; Rv413; Rv414; Rv415; Rv416; Rv417; Rv418; Rv419;  
 Rv41; Rv42; Rv43; Rv44; Rv45; Rv46; Rv47; Rv48; Rv49; Rv4; Rv50; Rv51;  
 Rv52; Rv53; Rv54; Rv55; Rv56; Rv57; Rv58; Rv59; Rv5; Rv60; Rv61; Rv62;  
 Rv63; Rv64; Rv65; Rv66; Rv67; Rv68; Rv69; Rv6; Rv70; Rv71; Rv72; Rv73;  
 Rv74; Rv75; Rv76; Rv77; Rv78; Rv79; Rv7; Rv80; Rv81; Rv82; Rv83; Rv84;  
 15 Rv85; Rv86; Rv87; Rv88; Rv89; Rv8; Rv90; Rv91; Rv92; Rv94; Rv95; Rv96;  
 Rv9.

The end sequences of the polynucleotide inserts of each of the above clones corresponding respectively to the sequences adjacent to the T7 promoter and to the Sp6 promoter on the BAC vector are shown in Table 3.

20 It has been shown by the inventors that the minimal overlapping set of BAC vectors of the BAC-based DNA library I-1945 contains 68 unique BAC clones and practically spans almost the whole H37Rv chromosome with the exception of a single gap of approximately 150 kb.

25 More specifically, a recombinant BAC vector of interest is chosen among the following set or group of BAC vectors from the BAC-based DNA library I-1945, the location of which vector DNA inserts on the chromosome of *M. tuberculosis* is shown in Figure 3 :

Rv234; Rv351; Rv166; Rv35; Rv415; Rv404; Rv209; Rv272; Rv30; Rv228;  
 Rv233; Rv38; Rv280; Rv177; Rv48; Rv374; Rv151; Rv238; Rv156; Rv92; Rv3;  
 30 Rv403; Rv322; Rv243; Rv330; Rv285; Rv233; Rv219; Rv416; Rv67; Rv222;  
 Rv149; Rv279; Rv87; Rv273; Rv266; Rv25; Rv136; Rv414; Rv13; Rv289; Rv60;  
 Rv104; Rv5; Rv165; Rv215; Rv329; Rv240; Rv19; Rv74; Rv411; Rv167; Rv56;  
 Rv80; Rv164; Rv59; Rv313; Rv265; Rv308; Rv220; Rv258; Rv339; Rv121;  
 Rv419; Rv418; Rv45; Rv217; Rv134; Rv17; Rv103; Rv21; Rv22; Rv2; Rv270;  
 35 Rv267; Rv174; Rv257; Rv44; Rv71; Rv7; Rv27; Rv191; Rv230; Rv128; Rv407;

N 21.06.00

18

Rv106; Rv39; Rv255; Rv74; Rv355; Rv268; Rv58; Rv173; Rv264; Rv417; Rv401; Rv144; Rv302; Rv81; Rv163; Rv281; Rv221; Rv420; Rv175; Rv86; Rv412; Rv73; Rv269; Rv214; Rv287; Rv42; Rv143.

5 The polynucleotides disclosed in Table 3 may be used as probes in order to select a given clone of the BAC DNA library I-1945 for further use.

The invention also provides for a BAC-based *Mycobacterium bovis* strain Pasteur genomic DNA library that has been deposited in the Collection Nationale de Cultures de Microorganismes on June 30, 1998 under the accession number I-2049.

10 A further object of the invention consists in a recombinant BAC vector which is chosen among the group consisting of the recombinant BAC vectors belonging to the BAC-based DNA library I-2049. This DNA library contains approximately 1600 clones. The average insert size is estimated to be ~80 kb.

15 Generally, a recombinant BAC vector of interest may be chosen among the following set or group of BAC vectors contained in the BAC-based DNA library I-2049 :

X0001; X0002; X0003; X0004; X0006; X0007; X0008; X0009; X0010; X0012; X0013; X0014; X0015; X0016; X0017; X0018; X0019; X0020; X0021; X0175.

20 The end sequences of the polynucleotide inserts of each of the above clones corresponding respectively to the sequences adjacent to the T7 promoter and to the Sp6 promoter on the BAC vector are shown in Table 4.

The polynucleotides disclosed in Table 4 may be used as probes in order to select a given clone of the BAC DNA library I-2049 for further use.

25 Are also part of the invention the polynucleotide inserts that are contained in the above described BAC vectors, that are useful as primers or probes.

These polynucleotides and nucleic acid fragments may be used as primers for use in amplification reactions, or as nucleic probes.

30 PCR is described in the US patent N° 4,683,202. The amplified fragments may be identified by an agarose or a polyacrylamide gel electrophoresis, or by a capillary electrophoresis or alternatively by a chromatography technique (gel filtration, hydrophobic chromatography or ion exchange chromatography). The specificity of the amplification may be ensured by a molecular hybridization using, for example, one of the initial primers as nucleic probes.

35 Amplified nucleotide fragments are used as probes in hybridization reactions in order to detect the presence of one polynucleotide according to the

present invention or in order to detect mutations in the genome of the given mycobacterium of interest, specifically a mycobacterium belonging to the *Mycobacterium tuberculosis* complex and more specifically *Mycobacterium tuberculosis* and *Mycobacterium bovis* BCG.

- 5 Are also part of the present invention the amplified nucleic fragments (« amplicons ») defined herein above.

These probes and amplicons may be radioactively or non-radioactively labeled, using for example enzymes or fluorescent compounds.

- 10 Other techniques related to nucleic acid amplification may also be used and are generally preferred to the PCR technique.

- The Strand Displacement Amplification (SDA) technique (Walker et al., 1992) is an isothermal amplification technique based on the ability of a restriction enzyme to cleave one of the strands at his recognition site (which is under a hemiphosphorothioate form) and on the property of a DNA polymerase to initiate the synthesis of a new strand from the 3'OH end generated by the restriction enzyme and on the property of this DNA polymerase to displace the previously synthesized strand being localized downstream. The SDA method comprises two main steps :

- 15 a) The synthesis, in the presence of dCTP- $\alpha$ -S, of DNA molecules that are flanked by the restriction sites that may be cleaved by an appropriate enzyme.
- 20 b) The exponential amplification of these DNA molecules modified as such, by enzyme cleavage, strand displacement and copying of the displaced strands. The steps of cleavage, strand displacement and copy are repeated a sufficient number of times in order to obtain an accurate sensitivity of the assay.

- 25 The SDA technique was initially realized using the restriction endonuclease HincII but is now generally practised with an endonuclease from *Bacillus stearothermophilus* (BSOI) and a fragment of a DNA polymerase which is devoid of any 5'→3' exonuclease activity isolated from *Bacillus cladothex* (exo- Bca) [=exo-minus-Bca]. Both enzymes are able to operate at
- 30 60°C and the system is now optimized in order to allow the use of dUTP and the decontamination by UDG. When using this technique, as described by Spargo et al. in 1996, the doubling time of the target DNA is of 26 seconds and the amplification rate is of  $10^{10}$  after an incubation time of 15 min at 60°C.

The SDA amplification technique is more easy to perform than PCR (a single thermostated waterbath device is necessary) and is faster than the other amplification methods.

Thus, another object of the present invention consists in using the nucleic acid fragments according to the invention (primers) in a method of DNA or RNA amplification according to the SDA technique. For performing SDA, two pairs of primers are used : a pair of external primers (B1, B2) consisting of a sequence specific for the target polynucleotide of interest and a pair of internal primers (S1, S2) consisting of a fusion oligonucleotide carrying a site that is recognized by a restriction endonuclease, for example the enzyme BSOBI.

The operating conditions to perform SDA with such primers are described in Spargo et al, 1996.

The polynucleotides of the invention and their above described fragments, especially the primers according to the invention, are useful as technical means for performing different target nucleic acid amplification methods such as :

- TAS (Transcription-based Amplification System), described by Kwoh et al. in 1989.
- SR (Self-Sustained Sequence Replication), described by Guatelli et al. in 1990.
- NASBA (Nucleic acid Sequence Based Amplification), described by Kievitis et al. in 1991.
- TMA (Transcription Mediated Amplification).

The polynucleotides according to the invention are also useful as technical means for performing methods for amplification or modification of a nucleic acid used as a probe, such as :

- LCR (Ligase Chain Reaction), described by Landegren et al. in 1988 and improved by Barany et al. in 1991 who employ a thermostable ligase.
- RCR (Repair Chain Reaction) described by Segev et al. in 1992.
- CPR (Cycling Probe Reaction), described by Duck et al. in 1990.
- Q-beta replicase reaction, described by Miele et al. in 1983 and improved by Chu et al. in 1986, Lizardi et al. in 1988 and by Burg et al. and Stone et al. in 1996.

When the target polynucleotide to be detected is a RNA, for example a mRNA, a reverse transcriptase enzyme will be used before the amplification reaction in order to obtain a cDNA from the RNA contained in the biological sample. The generated cDNA is subsequently used as the nucleic acid target for

the primers or the probes used in an amplification process or a detection process according to the present invention.

The non-labeled polynucleotides or oligonucleotides of the invention may be directly used as probes. Nevertheless, the polynucleotides or oligonucleotides  
5 are generally labeled with a radioactive element ( $^{32}\text{P}$ ,  $^{35}\text{S}$ ,  $^3\text{H}$ ,  $^{125}\text{I}$ ) or by a non-isotopic molecule (for example, biotin, acetylaminofluorene, digoxigenin, 5-bromodesoxyuridin, fluorescein) in order to generate probes that are useful for numerous applications.

Examples of non-radioactive labeling of nucleic acid fragments are  
10 described in the french patent N° FR-7810975 or by Urdea et al. or Sanchez-Pescador et al., 1988.

In the latter case, other labeling techniques may be also used such as those described in the french patents FR-2 422 956 and 2 518 755. The hybridization  
15 step may be performed in different ways (Matthews et al., 1988). The more general method consists of immobilizing the nucleic acid that has been extracted from the biological sample onto a substrate (nitrocellulose, nylon, polystyrene) and then to incubate, in defined conditions, the target nucleic acid with the probe. Subsequently to the hybridization step, the excess amount of the specific probe is discarded and the hybrid molecules formed are detected by an appropriate  
20 method (radioactivity, fluorescence or enzyme activity measurement).

Advantageously, the probes according to the present invention may have structural characteristics such that they allow the signal amplification, such structural characteristics being, for example, branched DNA probes as those described by Urdea et al. in 1991 or in the European patent N° EP-0 225 807  
25 (Chiron).

In another advantageous embodiment of the probes according to the present invention, the latters may be used as « capture probes », and are for this purpose immobilized on a substrate in order to capture the target nucleic acid contained in a biological sample. The captured target nucleic acid is subsequently  
30 detected with a second probe which recognizes a sequence of the target nucleic acid which is different from the sequence recognized by the capture probe.

The oligonucleotide probes according to the present invention may also be used in a detection device comprising a matrix library of probes immobilized on a substrate, the sequence of each probe of a given length being localized in a shift  
35 of one or several bases, one from the other, each probe of the matrix library thus

being complementary to a distinct sequence of the target nucleic acid. Optionally, the substrate of the matrix may be a material able to act as an electron donor, the detection of the matrix poisons in which an hybridization has occurred being subsequently determined by an electronic device. Such matrix libraries of probes and methods of specific detection of a target nucleic acid is described in the European patent application N° EP-0 713 016 (Affymax technologies) and also in the US patent N° US-5,202,231 (Drmanac).

Since almost the whole length of a mycobacterial chromosome is covered by a BAC-based genomic DNA libraries according to the present invention (i.e. 97% of the *M. tuberculosis* chromosome is covered by the BAC library I-1945), these DNA libraries will play an important role in a plurality of post-genomic applications, such as in mycobacterial gene expression studies where the canonical set of BACs could be used as a matrix for hybridization studies. Probing such matrices with cDNA probes prepared from total mRNA will uncover genetic loci induced or repressed under different physiological conditions (Chuang et al., 1993; Trieselmann et al., 1992). As such, the H37Rv BAC library represents a fundamental resource for present and future genomics investigations.

The BAC vectors or the polynucleotide inserts contained therein may be directly used as probes, for example when immobilized on a substrate such as described herein before.

The BAC vectors or their polynucleotide inserts may be directly adsorbed on a nitrocellulose membrane, at predetermined locations on which one or several polynucleotides to be tested are then put to hybridize therewith.

Preferably, a collection of BAC vectors that spans the whole genome of the mycobacterium under testing will be immobilized, such as, for example, the set of 68 BAC vectors of the I-1945 DNA library that is described elsewhere in the specification and shown in Figure 3.

The immobilization and hybridization steps may be performed as described in the present Materials and Methods Section.

As another illustrative embodiment of the use of the BAC vectors of the invention as polynucleotide probes, these vectors may be useful to perform a transcriptional activity analysis of mycobacteria growing in different environmental conditions, for example under conditions in which a stress response is expected, as it is the case at an elevated temperature, for example 40°C.



In this specific embodiment of the invention, Genescreen membranes may be used to immobilize the restriction endonuclease digests (*Hind*III digests for the BAC DNA library I-1945) of the BAC vectors by transfer from a gel (Trieselmann et al., 1992).

Alternatively, the BAC vectors may be immobilized for dot blot experiments as follows. First, the DNA concentration of each BAC clone is determined by hybridization of blots of clone DNAs and of a BAC vector concentration standard with a BAC vector specific DNA probe. Hybridization is quantified by the Betascope 603 blot analyzer (Betagen Corp.), which collects beta particles directly from the blot with high efficiency. Then, 0.5 µg of each clone DNA is incubated in 0.25 M NaOH and 10 mM EDTA at 65°C for 60 min to denature the DNA and degrade residual RNA contaminants. By using a manifold filtration system (21 by 21 wells), each clone DNA is blotted onto a GeneScreen Plus nylon membrane in the alkaline solution. After neutralization, the blots are baked at 85°C for 2 h under vacuum. Positive and negative controls are added when necessary. In order to perform this procedure, it may be referred to the article of Chuang et al. (1993).

For RNA extractions, cells grown in a suitable volume of culture medium may, for example, be immediately mixed with an equal volume of crushed ice at -70°C and spun at 4°C in a 50 ml centrifugation tube. The cell pellet is then suspended in 0.6 ml of ice-cold buffer (10 mM KCl, 5 mM MgCl, 10 mM Tris; pH 7.4) and then immediately added to 0.6 ml of hot lysis buffer (0.4 M NaCl, 40 mM EDTA, 1% beta-mercaptoethanol, 1% SDS, 20 mM Tris; pH 7.4) containing 100 µl of water saturated phenol. This mixture is incubated in a boiling water bath for 40 s. The debris are removed by centrifugation. The supernatant is extracted with phenol-chloroform five times, ethanol precipitated, and dried. The dried RNA pellet is dissolved in water before use.

Then labeled total cDNA may be prepared by the following method. The reaction mixture contains 15 µg of the previously prepared total RNA, 5 µg of pd(N<sub>6</sub>) (random hexamers from Pharmacia Inc.), 0.5 mM dATP, 0.5 mM dGTP and 0.5mM dTTP, 5µM dCTP, 100 µCi of [ $\alpha$ -<sup>32</sup>P]dCTP (3,000 Ci/mmol), 50 mM Tris-HCl (pH 8.3), 6 mM MgCl<sub>2</sub>, 40 mM KCl, 0.5 U of avian myeloblastosis virus reverse transcriptase (Life Science Inc.) in a total volume of 50 µl. The reaction is allowed to continue overnight at room temperature. EDTA and NaOH are then added to final concentrations of 50 mM and 0.25 M, respectively, and

the mixture is incubated at 65°C for 30 min to degrade the RNA templates. The cDNA is then ready to use after neutralization by adding Hcl and Tris buffer.

The hybridization step may be performed as described by Chuang et al. (1993) and briefly disclosed hereinafter. The DNA dot blot is hybridized to <sup>32</sup>P-labeled total cDNA in a solution containing 0.1% polyvinylpyrrolidone, 0.1% Ficoll, 0.1% sodium Pp, 0.1% bovine serum albumin, 0.5% SDS, 100 mM NaCl, and 0.1 mM sodium citrate, pH 7.2, at 65°C for 2 days and then washed with a solution containing 0.1% SDS, 100 mM NaCl, and 10 mM Na-citrate, pH 7.2. The same dot blot is used for hybridization with both control and experimental cDNAs, with an alkaline probe stripping procedure (soaked twice in 0.25M NaOH-0.75 M NaCl at room temperature, 30 min each, neutralized, and completely dried at 65°C for at least 30 min) between the two hybridizations. Quantification may be done with the Betascope 603 blot analyzer (Betagen Corp.).

As it flows from the above technical teachings, another object of the invention consists in a method for detecting the presence of mycobacteria in a biological sample comprising the steps of :

- a) bringing into contact the recombinant BAC vector or a purified polynucleotide according to the invention with a biological sample ;
- b) detecting the hybrid nucleic acid molecule formed between said purified polynucleotide and the nucleic acid molecules contained within the biological sample.

The invention further deals with a method for detecting the presence of mycobacteria in a biological sample comprising the steps of :

- a) bringing into contact the recombinant BAC vector or a purified polynucleotide according to the invention that has been immobilized onto a substrate with a biological sample ;
- b) bringing into contact the hybrid nucleic acid molecule formed between said purified polynucleotide and the nucleic acid contained in the biological sample with a labeled recombinant BAC vector or a polynucleotide according to the invention, provided that said polynucleotide and polynucleotide of step a) have non-overlapping sequences.

Another object of the invention consists in a method for detecting the presence of mycobacteria in a biological sample comprising the steps of :

- a) bringing into contact the nucleic acid molecules contained in the biological sample with a pair of primers according to the invention;  
b) amplifying said nucleic acid molecules;  
c) detecting the nucleic acid fragments that have been amplified, for example by gel electrophoresis or with a labeled polynucleotide according to the invention.

In one specific embodiment of the above detection and/or amplification methods, said methods comprise an additional step wherein before step a), the nucleic acid molecules of the biological sample have been made available to a hybridization reaction.

- 10 In another specific embodiment of the above detection methods, said methods comprise an additional step, wherein, before the detection step, the nucleic acid molecules that are not hybridized with the immobilized purified polynucleotide are removed.

Also part of the invention is a kit for detecting mycobacteria in a biological sample comprising :

- 15 a) a recombinant BAC vector or a purified polynucleotide according to the invention;  
b) reagents necessary to perform a nucleic acid hybridization reaction.

The invention also pertains to a kit for detecting a mycobacteria in a biological sample comprising :

- 20 a) a recombinant BAC vector or a purified polynucleotide according to the invention that is immobilized onto a substrate;  
b) reagents necessary to perform a nucleic acid hybridization reaction;  
c) a purified polynucleotide according to the invention which is radioactively or non-radioactively labeled, provided that said polynucleotide and the polynucleotide of step a) have non-overlapping sequences.

Moreover, the invention provides for a kit for detecting mycobacteria in a biological sample comprising :

- 25 a) a pair of purified primers according to the invention;  
b) reagents necessary to perform a nucleic acid amplification reaction;  
c) optionally, a purified polynucleotide according to the invention useful as a probe.

The invention embraces also a method for detecting the presence of a genomic DNA, a cDNA or a mRNA of mycobacteria in a biological sample, comprising the steps of :

- a) bringing into contact the biological sample with a plurality of BAC vectors according to the invention or purified polynucleotides according to the invention, that are immobilized on a substrate;
- b) detecting the hybrid complexes formed.

- 5       The invention also provides a kit for detecting the presence of genomic DNA, cDNA or mRNA of a mycobacterium in a biological sample, comprising :
- a) a substrate on which a plurality of BAC vectors according to the invention or purified polynucleotides according to the invention have been immobilized;
  - b) optionally, the reagents necessary to perform the hybridization reaction.

- 10       Additionally, the recombinant BAC vectors according to the invention and the polynucleotide inserts contained therein may be used for performing detection methods based on « molecular combing ». Said methods consist in methods for aligning macromolecules, especially DNA and are applied to processes for detecting, for measuring intramolecular distance, for separating and/or for
- 15       assaying a macromolecule, especially DNA in a sample.

- These « molecular combing » methods are simple methods, where the triple line S/A/B (meniscus) resulting from the contact between a solvent A and the surface S and a medium B is caused to move on the said surface S, the said macromolecules (i.e. DNA) having a part, especially an end, anchored on the
- 20       surface S, the other part, especially the other end, being in solution in the solvent A. These methods are particularly fully described in the PCT Application n° PCT/FR 95/00165 files on February 11, 1994 (Bensimon et al.).

- When performing the « molecular combing » method with the recombinant BAC vectors according to the inventions or their polynucleotide inserts, the
- 25       latters may be immobilized (« anchored ») on a suitable substrate and aligned as described in the PCT Application n° PCT/FR 95/00165, the whole teachings of this PCT Application being herein incorporated by reference. Then, polynucleotides to be tested, preferably under the form of radioactively or non radioactively labeled polynucleotides, that may consist of fragments of genomic
- 30       DNA, cDNA etc. are brought into contact with the previously aligned polynucleotides according to the present invention and then their hybridization position on the aligned DNA molecules is determined using any suitable means including a microscope or a suitable camera device.

- Thus, the present invention is also directed to a method for the detection
- 35       of the presence of a polynucleotide of mycobacterial origin in a biological sample

and/or for physical mapping of a polynucleotide on a genomic DNA, said method comprising :

- a) aligning at least one polynucleotide contained in a recombinant BAC vector according to the invention on the surface of a substrate;
- 5 b) bringing into contact at least one polynucleotide to be tested with the substrate on which the at least one polynucleotide of step a) has been aligned;
- c) detecting the presence and/or the location of the tested polynucleotide on the at least one aligned polynucleotide of step a).

The invention finally provides for a kit for performing the above method, comprising :

- a) a substrate whose surface has at least one polynucleotide contained in a recombinant BAC vector according to the invention;
- b) optionally, reagents necessary for labeling DNA;
- c) optionally, reagents necessary for performing a hybridization reaction.

In conclusion, it may be underlined that the alliance of such BAC-based approaches such as described in the present specification to the advances in comparative genomics by the availability of an increased number of complete genomes, and the rapid increase of well-characterized gene products in the public databases, will allow the one skilled in the art an exhaustive analysis of the mycobacterial genome.

## MATERIALS AND METHODS

1. **DNA-preparation.** Preparation of *M. tuberculosis* H37Rv DNA in agarose plugs was conducted as previously described (Canard et al., 1989; Philipp et al., 1996b). Plugs were stored in 0.2 M EDTA at 4°C and washed 3 times in 0.1% Triton X-100 buffer prior to use.
2. **BAC vector preparation.** pBeloBAC11 was kindly provided by Dr. Shizuya, Department of Biology, California Institute of Technology (Pasadena, CA). The preparation followed the description of Woo et al., 1994 (Woo et al., 1994).
3. **Partial digestion with *HindIII*.** Partial digestion was carried out on plugs, each containing approximately 10 µg of high molecular weight DNA, after three one hour equilibration steps in 50 ml of *HindIII* 1X digestion buffer (Boehringer Mannheim, Mannheim, Germany) plus 0.1% Triton X-100. The buffer was then removed and replaced by 1ml/plug of ice-cold *HindIII* enzyme buffer containing 20 units of *HindIII* (Boehringer). After two hours incubation on ice, the plugs

were transferred to a 37°C water bath for 30 minutes. Digestions were stopped by adding 500 µl of 50 mM EDTA (pH 8.0).

4. **Size selection.** The partially digested DNA was subjected to contour-clamped homogenous electric field (CHEF) electrophoresis on a 1% agarose gel using a  
5 BioRad DR III apparatus (BioRad, Hercules, CA) in 1X TAE buffer at 13°C, with a ramp from 3 to 15 seconds at 6 V/cm for 16 hours. Agarose slices from 25 to 75 kb, 75 to 120 kb and 120 to 180 kb were excised from the gel and stored in TE at 4°C.

5. **Ligation and transformation.** Agarose-slices containing fractions from 25 to  
10 75 kb, 75 to 120 kb and 120 to 180 kb were melted at 65°C for 10 minutes and digested with Gelase (Epicentre Technologies, Madison, WI), using 1 unit per 100 µl gel-slice. 25-100 ng of the size-selected DNA was then ligated to 10 ng of *Hind*III digested, dephosphorylated pBeloBAC11 in a 1:10 molar ratio using 10 units of T4 DNA ligase (New England Biolabs, Beverly, MA) at 16°C for 20  
15 hours. Ligation mixtures were heated at 65°C for 15 minutes, then drop-dialysed against TE using Millipore VS 0.025 mM membranes (Millipore, Bedford, MA). Fresh electrocompetent *E. coli* DH10B cells (Sheng et al., 1995) were harvested from 200 ml of a mid-log (OD<sub>550</sub>=0.5) culture grown in SOB medium. Cells were washed three times in ice-cold water, and finally resuspended in ice-cold  
20 water to a cell density of 10<sup>11</sup> cells/ml (OD<sub>550</sub>=150). 1 µl of the ligation-mix was used for electroporation of 30 µl of electrocompetent DH10B *E. coli* using a Eurogentec Easyject Plus electroporator (Eurogentec, Seraing, Belgium), with settings of 2.5 kV, 25 µF, and 99 Ω, in 2 mm wide electroporation cuvettes. After electroporation, cells were resuspended in 600 µl of SOC medium, allowed to  
25 recover for 45 minutes at 37°C with gentle shaking, and then plated on LB agar containing 12.5 µg/ml chloramphenicol (CM), 50 µg/ml X-gal, and 25 µg/ml IPTG. The plates were incubated overnight and recombinants (white colonies) were picked manually to 96 well plates. Each clone was inoculated 3 times (2 X 200 µl and 1 X 100 µl of 2YT/12.5 µg/ml CM per clone) and incubated  
30 overnight. One of the microtiter plates, containing 100 µl culture per well, was maintained as a master plate at -80°C after 100 ml of 80% glycerol were added to each well, while minipreps (Sambrook et al., 1989) were prepared from the remaining two plates to check for the presence of inserts. Clones containing inserts were then designated "Rv" clones, repicked from the master plate to a  
35 second set of plates for storage of the library at -80°C.

6. **Preparation of DNA for sizing, direct sequencing and comparative genomics.** A modified Birnboim and Doly protocol (Birnboim et al., 1979) was used for extraction of plasmid DNA for sequencing purposes. Each Rv clone was inoculated into a 50 ml Falcon polypropylene tube containing 40 ml of 2YT medium with 12.5 µg/ml of CM and grown overnight at 37°C with shaking. Cells were harvested by centrifugation and stored at -20°C. The frozen pellet was resuspended in 4 ml of Solution A (50 mM glucose, 10 mM EDTA, 25 mM Tris, pH 8.0) and 4 ml of freshly prepared solution B (0.2 M NaOH, 0.2% SDS) was then added. The solution was gently mixed and kept at room temperature for 5 minutes before adding 4 ml of ice-cold solution C (3M Sodium Acetate, pH 4.7). Tubes were kept on ice for 15 min, and centrifuged at 10,000 rpm for 15 min. After isopropanol precipitation, the DNA pellet was dissolved in 600 µl RNase solution (15 mM Tris HCl pH 8.0, 10 µg/ml RNase A). After 30 minutes at 37°C the DNA solution was extracted with chloroform:isoamylalcohol (24:1) and precipitated from the aqueous phase using isopropanol. The DNA pellet was then rinsed with 70% ethanol, air-dried and dissolved in 30 µl distilled water. In general, DNA prepared by this method was clean and concentrated enough to give good quality results by automatic sequencing (at least 300 bp of sequence). For a few DNA preparations, an additional polyethylene glycol (PEG) precipitation step was necessary, which was performed as follows. The 30 µl of DNA solution were diluted to 64µl, mixed gently and precipitated using 16 µl 4M NaCl and 80 µl of 13% PEG 8000. After 30 min on ice the tubes were centrifuged at 4°C, the pellet carefully rinsed with 70% ethanol, air-dried and diluted in 20 µl of distilled water.
7. **Sizing of inserts.** Insert sizes were determined by pulsed-field gel electrophoresis (PFGE) after cleavage with *DraI* (Promega). 100-200 ng of DNA was *DraI*-cleaved in 20 µl total reaction volume, following the manufacturer's recommendations, then loaded onto a 1% agarose gel and migrated using a pulse of 4 s for 15 h at 6.25 V/cm at 10°C on an LKB-Pharmacia CHEF apparatus. Mid-range and low-range PFGE markers (New England Biolabs) were used as size standards. Insert sizes were estimated after ethidium bromide staining of gels.
8. **Direct sequencing.** For each sequencing reaction 7 µl BAC DNA (300-500ng), 2 µl primer (2 µM), 8 µl reaction mix of the *Taq* DyeDeoxy Terminator cycle sequencing kit (Applied Biosystems) and 3 µl distilled water were used.

After 26 cycles (96°C for 30 sec; 56°C for 15 sec; 60°C for 4 min) in a thermocycler (MJ-research Inc., Watertown, MA) DNA was precipitated using 70 µl of 70% ethanol/0.5 mM MgCl<sub>2</sub>, centrifuged, rinsed with 70% ethanol, dried and dissolved in 2 µl of formamide/EDTA buffer. SP6 and T7 samples of 32 BAC clones were loaded onto 64 lane, 6% polyacrylamide gels and electrophoresis was performed on a Model 373A automatic DNA sequencer (Applied Biosystems) for 12 to 16 hours. The sequences of oligonucleotides used as primers are shown in Table 1.

9. **DOP-PCR.** As an alternate procedure we used partially degenerate oligonucleotides in combination with vector-specific (SP6 or T7) primers to amplify insert ends of BAC clones, following a previously published protocol for P1 clones (Liu et al., 1995). The degenerate primers Deg2, Deg3, Deg4, Deg6 (Table 1) gave the best results for selected amplification of insert termini.

**Table 1: Primers used for PCRs and sequencing**

Vector specific Primers for DOP PCR- first amplification step:

SP6-BAC1: AGT TAG CTC ACT CAT TAG GCA

T7-BAC1 : GGA TGT GCT GCA AGG CGA TTA

Vector specific Primers (direct sequencing, nested primer for second PCR step)

SP6 Mid: AAA CAG CTA TGA CCA TGA TTA CGC CAA

T7-Belo2: TCC TCT AGA GTC GAC CTG CAG GCA

Degenerate Primers:

Deg2: TCT AGA NNN NNN TCC GGC

Deg3: TCT AGA NNN NNN GGG CCC

Deg4: CGT TTA AAN NNN NWA GGC CG

Deg6: GGT ACT AGT NNN NNW TCC GGC

Primers used for the amplification of *M. bovis* DNA in polymorphic chromosomal region of Rv58:

Primer 1: ACG ACC TCA TAT TCC GAA TCC C

Primer 2: GCA TCT GTT GAG TAC GCA CTT CC

10. **Screening by pooled PCR.** To identify particular clones in the library which could not be detected by random end-sequencing of the 400 BAC clones, PCR-screening of DNA pools was performed. Primers were designed for regions of the chromosome where no BAC coverage was apparent using cosmid-or H37Rv



whole genome shotgun sequences. Primers were designed to amplify approximately 400-500 bp. Ninety-six-well plates containing 200  $\mu$ l 2YT/12.5  $\mu$ g/ml CM per well were inoculated with 5  $\mu$ l of -80°C glycerol stock cultures each from the master plates and incubated overnight. The 96 clones of each plate were pooled by taking 20  $\mu$ l of culture from each well and this procedure was repeated for 31 plates. Pooled cultures were centrifuged, the pellets were resuspended in sterile water, boiled for 5 minutes, centrifuged and the supernatants kept for PCRs. As an initial screening step, the 31 pools of a total of 2976 BACs, representing about two thirds of the library were tested for the presence of a specific clone using appropriate PCR primers. PCR was performed using 10  $\mu$ l of supernatant, 5  $\mu$ l of assay buffer (100 mM b-mercaptoethanol, 600 mM Tris HCl (pH 8.8), 20 mM MgCl<sub>2</sub>, 170 mM (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>), 5  $\mu$ l of Dimethylsulfoxide (DMSO), 5  $\mu$ l of dNTPs (20 mM), 5  $\mu$ l of water, 10  $\mu$ l primer (2  $\mu$ M), 10  $\mu$ l inverse primer (2  $\mu$ M) and 0.2 units of *Taq* DNA polymerase (Boehringer). 32 cycles of PCR (95°C for 30 s, 55°C for 1 min 30 s, 72°C for 2 min) were performed after an initial denaturation at 95°C for 1 min. An extension step at 72 °C for 5 min finished the PCR. If a pool of 96 clones yielded an appropriate PCR product (Fig. 1A), subpools were made to identify the specific clone. Subpools representative for lane A of a 96 well plate were made by pooling clones 1 to 12 from lane A into a separate tube. Subpools for lanes B to H were made in the same way. In addition, subpools of each of the 12 rows (containing 8 clones each) were made, so that for one 96 well plate, 20 subpools were obtained. PCR with these 20 subpools identified the specific clone (Fig. 1B, lower gel portion). If more than one specific clone was present among the 96 clones of one plate (Fig. 1B, upper gel portion), additional PCR reactions had to be performed with the possible candidates (data not shown).

**11. Genomic comparisons.** DNA from the BAC clone Rv58 was digested with the restriction endonucleases *Eco*RI and *Pvu*II, and resolved by agarose gel electrophoresis at low voltage overnight (1.5 V/cm). DNA was transferred via the method of Southern to nitrocellulose membranes (Hybond C extra, Amersham) following standard protocols (Sambrook et al., 1989), then fixed to the membranes at 80°C for 2 hours. The blot was hybridized with <sup>32</sup>P labelled total genomic DNA from *M. tuberculosis* H37Rv, *M. bovis* type strain (ATCC 19210) or *M. bovis* BCG Pasteur. Hybridization was performed at 37°C overnight in

50% formamide hybridization buffer as previously described (Philipp et al., 1996b). Results were interpreted from the autoradiograms.

**12. Computer analysis.** Sequence data from the automated sequencer ABI373A were transferred as binary data to a Digital Alpha 200 station or Sun SparcII station and analysed using TED, a sequence analysis program from the Staden software package (Dear et al., 1991). Proof-read sequences were compared using the BLAST programs (Altschul et al., 1990) to the *M. tuberculosis* H37Rv sequence databases of the Sanger Centre, containing the collected cosmid sequences (TB.dbs) and whole-genome shotgun reads (TB\_shotgun\_all.dbs) (http://www.sanger.ac.uk/). In addition, local databases containing 1520 cosmid end-sequences and the accumulating BAC end-sequences were used to determine the exact location of end-sequenced BACs on the physical and genetic map. MycDB (Bergh et al., 1994) and public databases (EMBL, Genbank) were also used to compare new sequences, but to a lesser extent. The organization of the open reading frames (ORFs) in the polymorphic region of clone Rv58 was determined using the DIANA software established at the Sanger Centre.

## EXAMPLES

**Example 1 : Construction of a pBeloBAC11 library of *M. tuberculosis* H37Rv.**

Partial *Hind*III fragments of H37Rv DNA in the size range of 25 to 180 kb were ligated into pBeloBAC11 and electroporated into strain *E. coli* DH10B. While cloning of fractions I (25 to 75 kb) and II (75 to 120 kb) gave approximately  $4 \times 10^4$  transformants (white colonies), cloning of fraction III (120 to 180 kb) repeatedly resulted in empty clones. Parallel cloning experiments using partial *Hind*III digests of human DNA resulted in stable inserts for all three fractions (data not shown), suggesting that the maximum size of large inserts in BAC clones is strongly dependent on the source of the DNA. Analysis of the clones for the presence of inserts revealed that 70 % of the clones had an insert of the appropriate size while the remaining 30% of white colonies represented empty or *lacZ'*-mutated clones. Size determination of randomly selected, *Dra*I-cleaved BACs via PFGE showed that the insert sizes ranged for the majority of the clones between 40 kb and 100 kb with an average size of 70 kb. Clones with inserts of appropriate size were designated with "Rv" numbers, recultured and stored at -80°C for further use.

**Example 2 : Direct DNA sequence analysis of BACs.**

To characterize the BAC clones, they were systematically subjected to insert termini sequencing. Two approaches, direct sequencing of BAC DNA and PCR with degenerate oligonucleotide primers (DOP), adapted to the high G+C content of mycobacterial DNA, were used. In a first screening phase, 50 BAC clones designated Rv1 to Rv50 were analysed using both methods in parallel. Except for two clones, where the sequences diverged significantly, the sequences obtained by the two methods only differed in length. Sequences obtained directly were on average about 350 bp long and for 95% of the clones both the SP6 and T7 end-sequences were obtained at the first attempt. Sequences obtained by DOP-PCR were mostly shorter than 300 bp. For 40% of the BACs we obtained only very short amplicons of 50 to 100 base pairs from one end. In two cases the sequence obtained with the DOP-PCR differed from the sequences obtained by direct sequencing, and in these cases *E. coli* or vector sequences were amplified (data not shown). Taking the advantages and disadvantages of both methods into account, we decided to use direct termini sequencing for the systematic determination of the SP6 and T7 end-sequences.

**Example 3 : Representativity of the library.**

After having determined the end-sequences of 400 BACs a certain redundancy was seen. The majority of clones were represented at least 3 to 4 times. Maximum redundancy was seen in the vicinity of the unique *rrn* operon, as 2.5 % of the clones carried identical fragments that bridge the cosmid Y50 and Y130 (Fig. 3, approximate position at 1440 kb). The majority of clones with identical inserts appeared as two variants, corresponding to both possible orientations of the *HindIII* fragment in pBeloBAC11. This suggests that the redundancy was not the result of amplification during library construction, but due to the limited number of possible combinations of partial *HindIII* fragments in the given size-range of 25 to 120 kb. To detect rare BAC clones, a pooled PCR protocol was used. Primers were designed on the basis of the existing cosmid sequences and used to screen 31 pools of 96 BAC clones. When positive PCR products of the correct size were obtained, smaller subpools (of 8 or 12 clones each) of the corresponding pool were subsequently used to identify the corresponding clone (Figs. 1A and 1B). With this approach 20 additional BACs (Rv401-Rv420) were found for the regions where no BACs were found with the initial systematic sequencing approach. The end-sequences of these BACs

(Rv401-420) were determined by direct sequencing, which confirmed the predicted location of the clones on the chromosome. A 97% coverage of the genome of H37Rv with BAC clones was obtained. Only one region of ~ 150 kb was apparently not represented in the BAC library as screening of all pools with several sets of specific primers did not reveal the corresponding clone. This was probably due to the fact that *Hind*III fragments of mycobacterial DNA larger than 110 kb are very difficult to establish in *E. coli* and that a *Hind*III fragment of ~120 kb is present in this region of the chromosome (data not shown).

**Example 4 : Establishing a BAC map.**

Using all end-sequence and shotgun-sequence data from the H37Rv genome sequencing project, most of the BAC clones could then be localized by sequence comparison on the integrated map of the chromosome of *M. tuberculosis* strain H37Rv (Philipp et al., 1996b) and an ordered physical map of the BAC-clones was established. PCR with primers from the termini sequences of selected BACs were used for chromosomal walking and confirmation of overlapping BACs (data not shown). The correct order of BACs on the map was also confirmed more recently, using 40,000 whole genome shotgun reads established at the Sanger Centre. In addition, pulsed-field gel electrophoresis of *Dra*I digests of selected BACs was performed (Fig. 2) in order to see if the approximate fragment size and the presence or absence of *Dra*I cleavage sites in the insert were consistent with the location of the BACs on the physical map (Fig. 3). Comparison of the sequence-based BAC-map with the physical and genetic map, established by PFGE and hybridization experiments (Philipp et al., 1996b), showed that the two maps were in good agreement. The positions of 8 genetic markers previously shown on the physical and genetic map were directly confirmed by BAC-end-sequence data (Table 2, Fig. 3). The position of 43 from 47 Y-clones (91%) shown on the physical and genetic map, which were later shotgun sequenced, was confirmed by the BAC end-sequences and shotgun sequence data. Four clones (Y63, Y180, Y251, and Y253) were located to different positions than previously thought and this was found to be due to book keeping errors or to chimeric inserts. Their present approximate location relative to the *oriC* is shown in Figure 3: Y63 at 380 kb, Y63A at 2300 kb, Y180 at 2160 kb, Y251 at 100 kb, and Y253 at 2700 kb. A total of 48 BACs, covering regions of the chromosome, not represented by cosmids were then shotgun sequenced (Cole et al., 1997), and these are squared in Fig. 3. No chimeric BACs

were found, which is consistent with the observations of other research groups for other BAC libraries (Cai et al., 1995; Zimmer et al., 1997). The absence of chimeric BACs was of particular importance for the correct assembly of the *M. tuberculosis* H37Rv sequence. The exact position of the BAC termini sequences on the chromosome will be available via the world wide web (<http://www.pasteur.fr/MycDB>).

Table 2 : Identities of genetic markers previously shown on the integrated and genetic map of H37Rv (Phlipp et al., 1996b) wich showed perfect sequence homology with BAC ens sequences.

Locus	BAC end sequence	Description of genetic marker	Organism	GenBank Accession n°
<i>apa</i>	Rv163SP6	Secreted alanine-proline-rich antigen	<i>M. tuberculosis</i>	X80268
<i>dnaJ, dnaK</i>	Rv164T7	DnaJ hsp	<i>M. leprae</i>	M95576
<i>fop-A</i>	Rv136T7	Fibronectin binding protein	<i>M. tuberculosis</i>	M27016
<i>polA</i>	Rv401T7	DNA polymerase I	<i>M. tuberculosis</i>	L11920
<i>ponA</i>	Rv273T7	Penicillin binding protein	<i>M. leprae</i>	S82044
<i>pslC</i>	Rv103T7	Putative phosphate transport receptor	<i>M. tuberculosis</i>	Z48057
<i>recA</i>	Rv415SP6	Homologous recombination	<i>M. tuberculosis</i>	X58485
<i>wag9</i>	Rv35SP6	35-kDa antigen	<i>M. tuberculosis</i>	M69187

#### Example 5 : Repetitive end-sequences.

Repetitive sequences can seriously confound mapping and sequence assembly. In the case of the BAC end-sequences, no particular problems with repetitive sequences were observed. Although nine clones with one end in an IS1081 (Collins et al., 1991) sequence were identified, it was possible to correctly locate their position on the map using the sequence of the second terminus. Moreover, these BACs were used to determine the exact locations of IS1081 sequences on the map. Five copies of this insertion sequence, which

harbors a *Hind*III cleavage site, were mapped on the previous physical and genetic map. In contrast, BAC end-sequence data revealed an additional copy of *IS1081* on the *M. tuberculosis* H37Rv chromosome. The additional copy was identified by six clones (Rv27, Rv118, Rv142, Rv160, Rv190, Rv371) which harbored an identical fragment linking Y50 to I364 (Fig. 3, at ~ 1380 kb). This copy of *IS1081* was not found by previous hybridization experiments probably because it is located near another copy of *IS1081*, localized on the same *Dra*I fragment Z7 and *Asn*I fragment U (Fig. 3, at ~ 1140 kb). Furthermore, the position of a copy of *IS1081* previously shown in *Dra*I fragment Y1 (Fig. 3, at ~ 1840 kb) had to be changed to the region of Y349 (Fig. 3, at ~ 3340 kb) according to the end-sequences of BAC Rv223. The positions of the four other *IS1081* copies were confirmed by the sequence data and therefore remained unchanged. In total 6 copies of *IS1081* were identified in the H37Rv genome in agreement with the findings of others (Collins et al., 1991).

In addition, a sequence of 1165 bp in length containing a *Hind*III site was found in two copies in the genome of H37Rv in different regions. The end-sequences of BAC clones Rv48 and Rv374, covering cosmid Y164, as well as Rv419 and Rv45, that cover cosmid Y92, had perfect identity with the corresponding parts of this 1165 bp sequence (Fig. 3, at ~ 3480 kb and ~ 900 kb). Analysis of the sequence did not reveal any homology with insertion sequences or other repetitive elements. However, as each of the two locations showed appropriate BAC coverage, chimerism of the sequenced cosmids Y164 and Y92 can be ruled out as the probable cause.

#### Example 6 : Using BAC clones in comparative genomics.

The minimal overlapping set of BAC clones represents a powerful tool for comparative genomics. For example, with each BAC clone containing on average an insert of 70 kb, it should be possible to cover a 1Mb section of the chromosome with 15 BAC clones. Restriction digests of overlapping clones can then be blotted to membranes, and probed with radiolabelled total genomic DNA from, for example, *M. bovis* BCG Pasteur. Restriction fragments that fail to hybridize with the *M. bovis* BCG Pasteur DNA must be absent from its genome, hence identifying polymorphic regions between *M. bovis* BCG Pasteur and *M. tuberculosis* H37Rv. The results of such an analysis with clone Rv58 (Fig. 3, at ~1680 kb) are shown here. This clone covers a previously described polymorphic genomic region between *M. tuberculosis* and *M. bovis* BCG strains (Philipp et

al., 1996a). *Eco*RI and *Pvu*II digests from clone Rv58, fixed on nitrocellulose membranes, were hybridized with <sup>32</sup>P-labelled total genomic DNA from *M. tuberculosis* H37Rv, *M. bovis* (ATCC 19120), and *M. bovis* BCG Pasteur. Figures 4A and 4B present the results of this analysis, where it is clear that several restriction fragments from clone Rv58 failed to hybridize with genomic DNA from either *M. bovis* or *M. bovis* BCG Pasteur. On the basis of the various missing restriction fragments, a restriction map of the polymorphic region was established and compared to the H37Rv sequence data. The localization of the polymorphism could therefore be estimated, and appropriate oligonucleotide primers (Table 1) were selected for the amplification and sequencing of the corresponding region in *M. bovis*. The alignment of *M. bovis* and *M. tuberculosis* H37Rv sequences showed that 12,732 bp were absent from the chromosomal region of the *M. bovis* type strain and *M. bovis* BCG Pasteur strain. The G+C content of the polymorphic region is 62.3 mol%, which is the same as the average genome G+C content of the *M. tuberculosis* genome, hence indicating that this region is not a prophage or other such insertion. Subsequent PCR studies revealed that this segment was also absent from the Danish, Russian, and Glaxo substrains of *M. bovis* BCG, suggesting that this polymorphism can be used to distinguish *M. bovis* from *M. tuberculosis*. Analysis of this sequence showed that 11 putative open reading frames (ORFs) are present in *M. tuberculosis*, corresponding to ORFs MTCY277.28 to MTCY277.38 / accession number Z79701 -EMBL Nucleotide Sequence Data Library (Fig. 5). FASTA searches against the protein and nucleic acid databases revealed that the genes of this region may be involved in polysaccharide biosynthesis. Among these putative genes, the highest score was seen with ORF 6 (MTCY277.33), whose putative product shows a 51.9% identity with GDP-D-Mannose dehydratase from *Pseudomonas aeruginosa* (accession number U18320 - EMBL Nucleotide Sequence Data Library) in a 320 amino acid overlap. The novel *M. bovis* sequence of the polymorphic region was deposited under accession number AJ003103 in the EMBL Nucleotide Sequence Data Library.

As it appears from the teachings of the specification, the invention is not limited in scope to one or several of the above detailed embodiments; the present invention also embraces all the alternatives that can be performed by one skilled in the same technical field, without deviating from the subject or from the scope of the instant invention.

**Table 3 :** End-sequences of the polynucleotide inserts cloned in the named recombinant BAC vectors contained in the 1-1945 *M. tuberculosis* H37Rv genomic DNA library.

RvXXXSP6 corresponds to the SP6 end-sequence of the clone RvXXX.

RvXXXT7 corresponds to the T7 end-sequence of the clone RvXXX.

RvXXXIS 1081 corresponds to a region located close to a copy of the IS1081 repetitive sequence (Insertion element).

The character « - » denotes an uncertain base residue.

#### Clone Rv101

```

:-----:Rv101SP6.seq:-----:
AATACTCAAGCTTGGCCAGCGTCGATGACAAGAAATATGTCGCGAAAAGACTCAGCGGGCGACTTTGCTCGCAGCTG
CGGCTACCGCGCCACCGATTCTATGCGCGTGGTTCGCGGAAAAATGCTCCGAAAATCGCAGCGCCGACTCCAGTTTCGGC
GAGCATTCGGCGATGCCAGCTGCGGCTGCGCCCTGCCGGCCACGGCACCCACATGCGGCGATTCTGCTCCACCTGGGCGAG
CGCCCGCGCGCGAATTCCAACAATAGAATGCACCCGGGCGCGATCGTGGGTAAACAGCCAACGCCATGATCAGCGCT
CCGACGCGCGGTTGACTTGCCCGTTTGGCGTGCACCTACGAACGCGACATTGCGTTCGCGGCCCGGACAAAGTCGATCGT
GCGCGGCACCGCTGACTGCTTAACGGGCGATTGAAATCCGAT

```

#### -----:Rv101T7.seq:-----:

```

CCACCCGTGTAATTTGGGATGGGCAAAAAGCGGAAGCACCGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGG
TTAGGGCTTCTCGCGGGAAGGCCGGAACGTACGCGGTTTCAACACCTCGCGTCGCCCTCCGACCGCGAACATTCGGGG
ATGGCAGCAACCTGCTGGCAACCTGCGCCGGGCGATGATCTGCAGCGTCCGCGGGGTAGTCGCGCGCCGGGCGGCTAC
ACTCTGAAACGCGATGACCATCGATGTGTGGATGCGACATCCGACGCAACGGTTTCTTACACCGCGATATGTTGCGCT
CGCTGCCCGGTGACCGGT

```

#### Clone Rv102

```

:-----:Rv102SP6.seq:-----:
AATACTCAAGCTTTCCGCCGATACCCGCCATGTCGCGCACATCCAGGACTTCTGCGGGGGATCCCGCTGCACGCGCGGG
ATTCCCAAAGTGGCGATGATCGGGCGCGCTACGTCGTGGTGTACCTCGTCGGTAAACAGAAACCGAAGCGTATGACTC
GGTCGCGCGGTGGGCGACATGGTGGACACCAACCGCCACCGCGACGGGGTGAAGGCTATGTGACCGGTCGGCGAGC
ACTCATTGCCGACGAGCGCGGCGGAGACAAAAGTATCGCTTAAGGTACCGCGCATCACCAACATGTTGATCGCAGC
AATGTTGCTAGTGATCTACGCTCCGTAATTACCGGGTTT

```

#### -----:Rv102T7.seq:-----:

```

GTGCGGTTCCAACCCGAATTTGGCTTTGCGCGCCATCGGTGAGGACGGCGTCCGGGTGCTCAACGACGAGCTGCTCCGC
GGGACACACCTCGATGCTGCCCATGGACGCGGTCGAAACGACAGCTGATCGAGCTACAACGCCGCGCGGAACGC
TTCCGCGCGCGGCGTGACCGCATCCGTTGACCGGGCGGATCGCGGTGATGTCGATGACGCGCATCGCCACCGGAGCG
ACGGCCAGGCGGCGTGCCAGGTGCGCCGGGCGCACGCTGCGGACAAGGTGTTGCTGCGCGGTCCCGATCGGCCACGAC
GACATCGTGGCGAGATTGCGCGGTACGCCGATGAGGTGGT

```

#### Clone Rv103

```

:-----:Rv103SP6.seq:-----:

```

```

AATACTCAAGCTTTCCGCGGAACCGGACACATTGCGAATATTGATGACAAAAATAAAATCATTTGATGGTTTGAAGTAC
CAGGCCGATCAAGCTTCGCGGAGCAAAATTCGAATCAAGAGGCCCAAGCCCGTACCAATCAGCCCGGCAACGAGGGA
TTCCGTCATTATCAGCAAAATACTGCTCTCGGGTTACACCCAAACAGCGCAATATGCGGAAAAACCGTCCGCCGTTG
CAGGACATTAATGTCACGCTATTGTAGATAAAAAGATACCCAC

```

#### -----:Rv103T7.seq:-----:

```

TGCTCCGAAACCTGGGGGTGTCGCTGCTGATGACCGGCATACGGACATCTTCCCTGAGACCGCGCGTTCGAAAC
CAGCCAGCTGTCCATCATAGNGGTTCAACCCGGCGCAAGGGCGACGGCACGCCAAGTTTCGCCAGCGTTTAACTAGTG
CTGTTAGCTTCATTTGCTGCGATCAAAACAGCTGGTCCGCGGTAGGAACTGAATTTGAAACTCAACCGATTGTTGGTGC
CGCGTAGGTGCTTCGCTGCGGTGCGCTGCTGTTGTTGTCGCGTGTGTAACGACGACAAATGTGACCGGGGAGGTGCA
ACCACTGGCCAGGCGTCGGCAAAGGTGCTGATTCGGGGGGAAGAAGACACTCAAAGCCAGTGGGT

```



## Clone Rv104

.....Rv104SP6.seq:.....  
ATATCTCAAGCTTTGCCGACGAGCGGGCGATGTTGATGACGGGAAACCCAGCGCACACCGACGATTTTGGCGTAGCC  
GGCGGACGCTCTGCTCATTTCCGATACAGTCGGCGCTCGCATCGAGCATGGCGCGGCGACGGCTAGCAGCGATCCGCC  
GTCTCGAGGAGCAGCAGACGAGCCGTACGCCCGGCCGTAAGCCCGCGCCAGGATTCGGCGAAAACCGTTCTACGTG  
CGGGGTGATCTGGGTGTCGAATGATTCTGCGGGTGCCTAGCGCTCGCTGCAATCTCTCGACATAGATGCGCTCGGGCCG  
CATCGCTCGACAACCTCCGGGTGAGTGAATAGCATCTGCCGATCACCGCAGCGTTGCGCGGATGAGGCCGAACCCGA  
ATA

## .....Rv104T7.seq:.....

TCCTATGTCCCTGCCGAGCANGTGATCGAACCGGTTGACAGATTTGTCTATCTCCGGACCTGACGGTGAGGTCGAAGTT  
TCCAGGAATTCGGCAAATTCGGTAAGAGCCTGAAGAATTCGGTATCGCCGGACGAAATCTCGCAGCATACGGGGCG  
ATATACGCTTCGGGTTTACGAGATGTCGATGGGGCCGCTGAGGCTTCACGTCCATGGGCCACAAAGGATGTTGTCTCG  
CGCTACCGTTTTCTCGACGGGGTGTGGCGCTTGCTCG

## Clone Rv105

.....Rv105SP6.seq:.....  
ATATCTCAAGCTTGATTCCGCCGAAACCGACCGTGAGCACCCCGCCAGCCACCAGCTCGGGTCGGGCGCGGGGCCGCG  
CGCCCGAGGCTGCTCCGCTCGGTGATGGCAGCCACCGCAGACACCCCGGCTGCGCTACGTTAAACATTCAGCGCG  
GAGCTACATCCAGCTCGGCCCGCCAGTGTTTCGGCCCTCTTTCAGGTGCAAGTCTATACCGATATGCGCATCCGCGAC  
CGCCACCTCGAGAACAAGACATGCCCTACTAATGCTTGTCTGCGGGGCC

## .....Rv105T7.seq:.....

GGTACGCTTCGCTCGAGTCTCGCAGTGATGCATGACGACCGGGACCTCGTCGGCATCTTCCATAGCCGCCACACCT  
TCAGTTGCTCACCAGGAATCAACCCGGTAGAAGTTCGGCAGCGCTCGGCATTGCTCATCGGGATATGCCGCTCGGGAC  
GGTCAGAGCCCTCGGCTCCGGCCAGCACTCCGCGAGCTTCGTCGGGTGCTCGCGACGCGCATGGCCACCATCGCAT  
TCACAGGCTTCGGCGAATCACCAGCAGTAGACGGTTCCTTTCTTAAGCAACACCGAAGTTTCAGGACCCGAATGCT  
CCGGGAACATGTACGCTAGGTGCGGTATTCGGCTACCGGCTGA

## Clone Rv106

.....Rv106SP6.seq:.....  
GGCGTCAACGGTGTGGAACCCGCTCAAGCAATTTGGTAGGCTCGAGTCTGTGAATCAGGCCGACGCTGTGGCCGCC  
CGCGC

## .....Rv106T7.seq:.....

GGCTNGCGTACCCGGTACCGGCCGCGGCCCTACCAGTGCAGGAATGGAAGCGCAGTAAGCCCTCAACGCGCCACCG  
CTTTGGCCCGCGCGCGGGGTAGCGCATCGGCGGTGGCGGTGGGCGCGCGCATCGCACTCACCAGCGGCTTTCG  
AGCTTTGTCGATCAACCGCGCCAGCATGGTCGANGATGCAATTCGAGACCATATTCGAATTTGGTTTCATCGGGGGCCC  
CGATCCGATGCCCTCCAGTTTGGCTGAGCAACAGCGAGCTNTCGCGGGATCGATGGCCACGCGGTTTCAATGG  
CCGATGCTCGCTGCCCCCGCATGCGCTTTCGGGAGAACCGATCTAGCACCCGATCCGCGCAGCTNG

## Clone Rv107

.....Rv107T7D4.seq:.....  
CGTAATNTCCGCGCAGCANGACTTCTGGGGGGATCNGCTGACAGTGGTNGGATCCCAAATTCGGGATGATCGGGCC  
GCCNACGTCGTTGTGTACCTCNCNTGTCACAAACNAACCGAANCCTATGACTCGGTCCACCGGTCGGGCACATGGTG  
GACACCCACCCGCCACCCGNCGGGGTGAAGGCTATGTACCCGGTCGGGCAACACTCAATGCCGACAGGCCGANGCC  
GGACACNANAGTATCNCNTAAGCTCACCGCCGATCAGGACGATGCTGATCGNNAATGTITNCTANTGATCTATCGCTCCG  
TAATACATCGGCTTCTGCTCTGATCATGGTCCGACNGAACTCCGGCGCAATCCGCGGATTCATCGNCTTCTGCTCGCC  
ATTCACATATTTTCAGCTTTTCAGCTTTCAGCATTCGCAACNAACCTGCTGCTCATGGNATGCGCGGACACGGACTACCGATATC  
ATGCTCGCCGTTACACATCNCGCCACGCCGCGAAGACNGAAACGCTTCTACACATNTTNCGGGACGCCACTNAA  
CTTGTTTCNGGTTTGACATTGCGCGCATGNTGCCACGTTTGCCGGCTCCCCCTA

## Clone Rv108

.....Rv108T7D4.seq:.....  
TGAATTTCCGATCCCAAATCTCGGTCAGATACAGGTCGCCATACCCCTTACTTCGGCAACGCTGGGCGGATTTGGC  
CTGCGNCTCGACANACATCAGCACCATGAAATGCGCGCAATCTCGTTACGCAATCCATACCATCGACATTCG  
CGCATCGACATCCGCGCTTCNCCTTTAAACGG

## Clone Rv109

.....:Rv109SP6.seq.:.....  
AACAGCTATGACCATGNTTACGCCAAGCTATTAGGTAACTATANAATACTCAAGCTTTTACGGTGATCGCGCATC  
ACCTGTTTCATGAACGTGAAGCAGCGGCANCGCTTCCTTTTCGGCCGCAACATGAGCCAGCGCTTCGTCCGCGGTTCNGG  
TGCAGGTGCTCGGCGAGCTCGGGCCGCGACAGCCGCTGACCCGTGAACACAGCTTCCATATCCCGCGACNAACNACNCC  
AGTCCGCTACGTAAACCCCTCCGCGACTGTCCATGGACAACAGCGCGTTTCCACCGACCGGGCCCGGTGTGGGGTGT  
TTCGGCGACCGGCGAGCGAGGTGGTCCACACTGCCGACGGCGCGCGAGCCGTTACCGACCAAGCGCCGGAACAACT  
CGCGCGATCGCATACTCCAACCGGTTTCGGGTACTGCAGGTGAGTGGCTACCTCCTCNCNGCTCGGCGAAGTCT  
TGCTCCANACGTCGGAAGACGGGAAGGAACAGTTCA

## .....:Rv109T7.seq.:.....

GACCGNCCATGTTTCCCAATGTGGTGCCAGTNCGGNGGCTACGTGCCATCNANACACTGGCGCAGGCTATCGCACCC  
CGTTATCNGCTACGAACAATAATCNCGGTATGCGTCTTANCATGAGTCGGCGACGNCGATCATGGTCGACACCCAG  
ACNAAATACCGAGATCGCCNTCNAAGNCTGTGTGCCCGGATTATCANGACTGACCTCCTGGCTGACCGGNNGTGNTG  
GTCCGATGCTCGGCCCGCGCGGTGNTCGTGGTCGGCTCGGATAGCGAAGTACGCTAAATTCGTGGCAGCTCG  
AAAGGGTCTCGCGGTGCGGCTCTTTGCGCAAAACCATGCNATGTTACGGTCCCTCGGGTGCGGCTGCGCGCGCGC

## Clone Rv10

.....:Rv10SP6D2.seq.:.....  
GGGATGGGCGGCGCCGCTAAACTCTTCGTGTCCACTAATCCGGGAGGNGCAATCTCGGGCGTTATGGCTCAGCTC  
GCGTCGCCCTCCGACCGCGAATCTCGGAGTTGGCAGCAACCTGGTAGCACCTGGCCG

## .....:Rv10T7D4.seq.:.....

NCCGTGCTTGACAAGTAAATATGTCGCGAAAAGTCTCAGCGGCGGACTTTGCTCGCAGGTGGCGGTACCGGCCACCG  
AGTCGATGCGCTGGTCGCGGAAGAATGCTCCCGAAATCGCAGCGGCTTCCCNNTTTAAACGGA

## Clone Rv110

.....:Rv110SP6.seq.:.....  
TTTAGGTGACACATATAGAAATACTCAAGCTTTGGTCTAGCGGCGGAGCAGATACGGGTGTCAATTGCCCCCGGCGG  
CGGCTCTCCGGGAAATGGCGGGTCCCCGGTGGTTTGTCTGATGAGTGCTGAACCGTANTCGAAGTGGCGGCGTCA  
CTCCACCCANCCAGCAGGCGAGCGAAGCTGAATCCTCCAACCGGTTGTGNATCCGGAACAAGTTGGGGTGCCTTGG  
GGCAATGACAGGTGGCGGCTGCGTGGCTTCGGGTCCGCGGCGCGGAGTGCTGCTGTGGAGTCNCCGCTGGGCAATTCGGC  
NTTTTGTGGCGGCCGCGGTGGTNGGGGCGCAACAGGTTNCCNNGTGGGTCGGGCTCAACGGTTCNACGGGCGAAGCCG  
CGGTTTGGTTCACNCGGCGCTGGTTCGGATCGCGTTGGCGGTCNCGG

## .....:Rv110T7.seq.:.....

CTACACCATCGAATACGACGGCGTTCGCNACTTTCCGCGGTACCCGCTCAACTTTGTGTCGACCCCTCAACGCCATTGC  
CGGCACTTACTACGTGCATCCAACCTACTTATCCTGACGCGCGGAACAAATTGACGACGCGGTTCCGCTGACCAATAC  
GGTCGCTCCACAGTACGACCAAGTACTATCATTCGACGCGANAACTGCCGCTGCTAGAGCCACTGCGATCCGCTGCC  
GATCTGGGGAACCACTGGCGCAACTGGTTCAACCAAACCTTGAANGTGATTGTTAACTGGGCTACNCGGACCCGCG  
CTATGGTTATTCNACTCNCGCCCAATGTTGCGACTCCGTTGGGTTGTTCANAAAGTCNNCCCGGTGCTCATCGC  
CGAANCTCTCNTCCGGGACCCACAGGGAATCNGCNATTTTCNCTACAATCANCCACCTCCA

## Clone Rv111

.....:Rv111T7.seq.:.....  
GCATGATCGGCGACTTTCCGGCGCGCCGCGCATACGGCGGCGTACCGATCTCGCGTCATACACCCGCGGGTAACTCGC  
CGACGGTGCCGGTTTCGCGAGCCGAAAGTGACACTCTGATTGAATCGAGTTCCAGGTCCAGCGGGTGCGCGACCAACG  
GCGCGAGCTCAACGACGCTCAATCNGTTGTCGCTTTCTACGGTCACCGACCTTGGTGACCGTAGTTNCNCCG

## Clone Rv112

.....:Rv112SP6.seq.:.....  
GACACTATGAGAACTCAAGCTTGCCAACCGCGCAGCTGCATCCGGCGGCGANACTGCTCCGCCGACCACTACGAAC  
CAACCTCGGGTGCCGAGGCCATTGACGATGTGCTGGTCGGCGCCCGGAGTCCGCGCAACATCAACGCGCGGGGACCC  
ACGANGGCGCCCCACCTTCGACGGCGAGCATATTCCGGCGCGGCTCAGCGGGCGGGGGCTCGAANCAGCAGCAGCA  
TCAACGTNGTCACCCGGCGGTGACCGGCCGATCGTCACACCCCAAGCCCAATGGCCGTCTCTCAACNCGGCGCA  
CCCGGCCGCGATCGTCACAGGNCCTAAGGCCATTGCCGTCCTCCT

## .....:Rv112T7.seq.:.....

TGGGGCCGACCTCGGCACTTTAGAGACCTGTATTTCGAGCGCGTGGCCNACTGAGGTGGCGGTTGGACNAAGTGTGCA  
CCGGTTTGATCGCTCGGCTCTGCCGGATGCCACCCGCGCTGGTGGTCGATCCGCAANAGACAANTTGTGGTGA  
NCGCTTGCTGCTCGACACCTTACGAGTGGTGGCACCGGGACGCTTACTGCTGGCATGCTCGACCGCGCTGGCGCA  
CNACTCGACAGNTTACAGAAAGNTCGCCNCCCAATTGCCGCGNANTGTCTCGGNTCCCTTTACNCCCAATGGGCG  
TTTCCACGCGTTACGGGCGCCNCTGGCGGGGTCTNCTCCCAANTACACGACATGCGCCGTTTCCGGA

## Clone Rv113

```

:::Rv113SP6.seq:::

```

ATACTCAAGCTTTTATGGTGATCGCGCATCACCTGGTTCATGAAGTGAAGCAGCGCAGCGCTTCCTTTTCGGGCCGCA  
ACATGAGCCAGCCTCTCGTCGGCGGTTCGGTGCAGGTGCTCGGGCAGCTTCGGCCGCAACAGCCCCGGCTTGAAACCTG  
AAAACNCNGCTTTCCCATATCCCGCGCAGCAAGAACGCCAGTTCGCTACTTAAACCCCTCCGCGAACCTCCATGGACAA  
CAGCGCGTCTCTCCACCAACCGGGCCCGGGTGT

.....Rv113T7.seq.....

TCGGCTCAGGCCCGCGCTGCTGGTAGAGTCGCTGACCGGTCGAGGTTTCGACAATGTGGTGCCGGTTCGGCGGCTACGT  
GCCATCGAGACATCGGTCGACGAGCTCATCCGACCGGTTTCATCGGCTACGGAACAATTCGGCGGATGTTGTTTAGACATATC  
TCGCGCAGCATGCTCATGTGTGCACACCGCAGGAAAGACGCAATCGCGTCGAGCATGTGTGCGCGGAGATTATC  
AGGACTGACCTCCTGGCTGACCGGCATGTTTGGTCGCGATGCTTGGCGCCGCCGCGCGTGGTCGTGGTCGGCTCGGA  
TAGCGAGGTGACGCAATTCCTGTGGCAGCTCGAAAGGGTCTGCGCGTGCCGCTCTTTCGCGCAACAATAGCGCAGGT  
TACGGTTCGCGCGGGTTCGGCGCTGGCGCGCGCC

## Clone Rv114

```

:::Rv114SP6.seq:::

```

CAAGCTATTTAGTGACACATAGATACATCAAGCTTCGGGTCTACCGCGGCCGGGAGCATCGCACAGCGCTCAGCA  
CGCGGTTCCTAGACGCTCAAGCAGGTGGCGCAATGACGAAACCCGACCCGCGCGAACCCCGGCGCGCCGCGCCG  
GGCGCGCATCATGTCTGCTGTGGAGCGGCCCATCANACCTTGGGCGCGCTAGGAGNCGGTGGTACGAATGGG  
CTGGTCCCGGGACCGGGCAAGTTCGACCTCAACGGCCGACGCTTGGANGACTACTTCCCAAACAAAGGTGCACCGAG  
TTGTATCAAGGACCCCTGGTCCCTCGCTGGATCGGGTGGAAAGTTTCGACATCTTTGGCCACTTGGGCGGCGCGCGCT  
CGGGTCAAGCGCGGGCGTCCCTGGGTATCGCCGGGCGATTGATTCTGTGATCCCGGAGAAAGCC

```

.....Rv114T7.seq.....

```

CGGTGGCCACCGCTTCGTGGTGGCGCGCGCTGCACAATGACCGTGTCTGTCTTGTGACCAACAACGGCTCGGGCC  
GAGCCACGACACTCCAAAGCAACCTTCGGCGACCACTACGGCGCGCGGGTTGACCACTGGCCACCGCTCACCAAC  
GCAGGTCTCAAGAAACCGCTTCGCGCGGTGCACGAAGTAGCGCCCTTGACCGGACCGGCTTCAACGTTCTTGG  
AATCGCTTTGACGACACGCGTCCGCAACAGTTCGCGCTCCACGTTCTTACGACGACGATAGTAGTGGCTTACCCTTCC  
TGCAACCTTTTCAGCAATGGCAAGCTTGGGAAGGCANCTGATCTTCTTGGTG

## Clone Rv115

```

.....Rv115SP6.seq.....

```

CCAGCATATTATAGGTGACACTATAGAAATACTAAGCTTTTGGCTGGGTGCGCTTCAAAATCNGCGTGCACCGCTATAGG  
TGTCGANCACGCGGTGGCGCGCGCACCCCACTGGCCCGGGTGTTTTCGCCCCGAACCCGGATCATGGTGACGACAA  
GGANATTCCNCTCTTGATGCTGGATTGCGGACCGCAAGGACTCTANGAGTACTCTCCCGGGGTGGAAAGATGCG  
CCAAATCCCCCTCCTCCAACCTTCCNAACAATCATTCGCGTTCCNCNCTCCGGTGGNGGTAACCNCCAATAAAACC  
CTGCGGCC

```

:::Rv115T7.seq:::

```

SCCCAGCATGGCCATCCCCGAAGACATCATTTGGCCATGGCGGGGCTTAACAGGTTCCAGCCCCACACANTGCC  
 GCTCGAATCGCGGTGCAACCATTTTCGACGGCCGGCAGGAGAACGCACGGGAAGCCGCAAAAGGGCTCGAGTTTCCCGG  
 CTCCAATATGTGTGTCGCAACCGAGATGGCGGCTCNAAAACNCNCCGCAGTCACGGCCACCGACGGAGTGTGAAAGAC  
 GTGNTCAGCGCCGCCCATATGGGTTGCCAATCGGACGGAGCATGTATCCGCGCGCAACCGGACGGCGGTGTGATGCC  
 ACGTTCGCGCANGANGGCANACCCGCAATGCGAGGAAACCAAGAAATCTGGGCGCATTCACCTTCAACC

Clone Rv116

```

:::Rv116SP6.seq:::

```

ATATCAAGCTTGCCACGCCGTGATGACAAGAAATATGTCCGCAAAAGACTCAGCGGCCGACTTTGCTCGCAGCTGG  
CGGTACCGCGCCACCGAGTTCGATGCCGTGGTTCGCGGAAGATGCTCCCGAATTCGCACGGCCAAATTCATTCCGGGA  
AGCATCCGCAATGCCAGCTGCGGTTGCCCCCTGCCGGCGGACCGCACCACCTTGGCGGCATTGCGTCCACCTGGGGCAGC  
GCCCCGCGCCAAATTCAAACAATAAAAAATGACCCCGC

:::Rv116T7.seq:::

CCACCCGTTGATTTTGGGATGGGCAAAAGCGAAGCACCGCGTGGCCACGAACCGCGGGAGGGAACAATCTCGGGCCGG  
CTAGGGCTTCTCGCGGGAAGGCCGACAGTACGGCGTTTCAACACGTCGCGTCGCCCTCCGACCGCGAACAATCTCGGGG  
ATGGCAGCAACCTGGTAGCACCTGTGCCGGGCGATGATCTGCAGCGTCGCCCGGGGTAGTCGCCGCCCGGGCGGCTAC  
AGTCTGAACCGCGATGACCATCGATGTGGATGCAGCATCCGACGCAACGGTCTCTACACGGCGATATGTCGCCTC  
CCTGCCCGT

Clone Rv117

:::Rv117SP6D2.seq:::

CTGCCCATGTTTGGGACGCCCGACCGCGATGCTGGAGGCTACACGGCCCTTGGTGCCTGGCCAGGGCGACCGA  
GCGGCTGCAACTGGCGGCTTGGTGACCGCAATACCTACGCGACCCGACCCCTNTCNCAANAGGATNTTGTTCGGC  
GACCCNCTC

:::Rv117T7D4.seq:::

CCGACTTTCGCGGTACCCGCTCACTTTGTGTCGACCCCTCAACGCCATTGCGGGCCTACTACGTGCACTCCAAT  
ACTTCATCTGACGCCGGAACAAATTGACGACGGGTTCCGCTGACCAATACGGTCGGTCCACGATGACCCAGTACT  
ACATCATCTGCACGAGAACCTGCCGTGCTAGAGCACTGCGATCGGTGCCGATCTGGGGAAACCACTGGCGAAC  
TGGTTCAACCAAACTGAAGGTATTGTTAACTGGGCTACGCGACGCGCTT

Clone Rv118

:::Rv118SP6.seq:::

ATACTCAAGCTTTGTACACCAAGTGTTCGACGAGCGCTCCATCCGGCGAGTGGATACTCCAGCAGGTAGCAGGT  
CGCCACCAAGCTGGTCACTGCGCGTTCAGCTCGCTTGGCGCGCTGCAGCAGCCATTCCGGGAAATACCTGCCCTGGCG  
CAGCTTGGGGATCCCAACTTCAATGGTTGCGGCACGGGTGTCAAATTCACGGTGGCGTAGCCGTTGCCCTAATTGGA  
CGCTCATCTGCTTTCGCGGTACCCGCCGCCGACAGGGCTTCGGCTTACGCCCCATCAGGGCGCAATAAATCT  
CAAGAGCAC

:::Rv118T7.seq:::

GAGCGAGCTTCGCGCGCAATTCTACTAGCGAGAAGTCTGGCCCGATACGGATCTGACCGAAGTCGCTGCGGTGCAGCC  
CACCCTCATTGGCGATGGCGCCGACGATGGCGCTGGACCGATCTTGTGCCGCTTGCAGCGCGACGCGGTAGGTGG  
TCAAGTCCGCTACGCTTGGGCTTTCGCGACGGTCCCGACGCTGGTCCGCGTTGCGCGGAAGCGCGGCTCGG  
GTGCCATCAGGAATGCCCTACCGCCCGGGCACTGCACGGCGAGTCCCGCGGCGATGTACGATCCGGGACATCATGCT  
CTGCTTATATCTCTCGACCACTGCGCGGAACAGCTCGATTCGCGGACCGCCAGCGCATTTGGTGATGGAATCGGGCA  
ACTTGGCCACCGCTGGGTGTTGACATCTCTGACGGTGGGCAATTGCGGCTCGGTAGCTTTGCCGCGTAGCCTTTTC  
ATC

Clone Rv119

:::Rv119SP6.seq:::

ATACTCAAGCTTCACTGACAGGAGCAATTCGTCGGCGCGCTGTCAGTGGGTGGTGGCCGAGCTGGTGCACCA  
CTCAGGCCGCGGTACCGCGGTACCGCGCGGGGAGCAAACTCGCGCGGGCATGGCAACTTCTTCCGCGACCATCACCG  
CAGACGCCGCTTCGGACCCCTGCTGTCCACACACAGTTGGCCAACGCATTAATCACCCGCAAGCTTCCGGAATCCA  
CGCCCTGTTCCG

:::Rv119T7.seq:::

TCCATCACCGATGTGGCNGGAGCATGCCATGTCTCACTACCACTCCGGCCGTGGCGGTTGGCGGCCCGG  
GGGTCGCGCGAATCTGACGAGGCGGTCCGAGAAATCGCCANACCCCGCTGAACCGGACACCCGCTGTGGGAGA  
TGACTTCTGTTGAGGGCTTGCCAACCCGATCGCGTGGTTGCCAAATTCACCATGGTGGCTGACGGTGTG  
CTCGGCAACATGATGACGCGGGGATGGATCTGCCGCCGGGACGGAGTGGCGCGCTATGTGCTGACCCGCGCT  
CTACCAAGCGCA

Clone Rv11

:::Rv11SP6.seq:::

AGCTTTCGATTTGCTGAGTAATGTCCGCCAACGTCAACCAACCGGATGAATTCATCATGCCGCCAGGGCGGCCA  
ACCAATGGTGGCCGCGAGCGGCGAGTCTGATCGAGCGCGAGGTTGCCGGCCGCCAGTTGATTCACGAACAGGGTGA  
GGTCAATAGCGGGCAGGATAGTGACGAAGGCAAGACTCCATTCGCCGTGGAAGAAGTATCGAG

09673476.113000

.....:Rv11T7.seq:.....:

AGCTTCAGAAACAGGCTGTGTGGGGCGACCCGGCTCGCCGAGTTCTGCACGCACCGCCTCAAGTCGGGCCCCGACCCG  
CGGGCATCTCCCGGTTCAGCAGAGGGCCGCGGCCCGCCGCGCAGCGACGGCGTTCTCGGCAGTTTCGGCGTCAATGATGC  
TGACCTGATCGGGCACCCGGGCGTTCTCGGCGTCTCGCGTTCACTAATCGCGGTGCTCAGCAGCGTCTCGACAGCCCA  
CCACCCGAGTGGGCGACCGAGTGTCTCCACCACGGACCGCAGCGATGCCCGTC

Clone Rv120

.....:Rv120SP6.seq:.....:

ATACTCAAGCTTCAGTTCCTCCACGACGCGTTCCTCAATGAATTTCCCGATCCCAATCTCGGTTAGATACAGGTC  
GCCATACCCCTTACTTCGGAACAGCTGGGCGGATTGGCCCTGCCGCTGCACAAACCATCAACGCCCTTCAAAATGCCG  
GCAATCTGTTAGCCAATCCAT

.....:Rv120T7.seq:.....:

GCTCTACGCCCGCTACGGGTGCAACATGCATCCGAGCAGATGCTCGAGCGCGCACCCCACTCGCCGATGGCCGGAAAC  
CGGCTGGTTACCCGGGTGGCGGCTGACGTTCCGCGCGCAGGACATCNGCTGGGAAGGGGCGCTTGGCCACCGTCGTCNA  
AGACCAAATTCGAAGGTGTTCTGTCGTCTCTACGACATGACCCCGCGGACGAGAAGAACCTTGACCGGTGGGAAGG  
CTCCGAGTTTCGGTATCCACCAGAAGATCCGATGCCGCTGGAGCGCATTTCTCGGACACCACAACGGGATCCCGTTC  
TCG

Clone Rv121

.....:Rv121SP6.seq:.....:

ATACTCAAGCTTGCCAAAGAGACTCGTCCACCAAGCAGGACGCGACCGTCGAGGTGGCGATCCGGCTTGGCGTCGAC  
CGGGTAAGGCCAAACCATGATGTTTCGGGACCGGTCAACCTGCCCAACCCGGCACTGGTTAAGAACTGCCCGGTGCG  
GGTTTTCGCGGTTGTTGAAAGGCCAATGCCTGCTTTGCCGTTGGGGGCGGATGTTGTCGGGAGTGACAATCTGATCA  
AAAGGATTTCAGGCGGTTGGCTGGAATTCATGCCCAATCGCGACACCGG

.....:Rv121T7.seq:.....:

CCACGGCGTGGATCAAGTACGGGCCGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGCTGATGTGGCGGTTAGCGC  
CGGATTCCACCACATCCCTTTCGAAAGTCCGTTGGGTGCAATGATGTAGCGCTTCTCCCATCGAGATAGTGGAGCA  
ACGCAATCCGTGGCGTTCGGTTTCGGTCTGACTCGATGTGCGCGACCTTGGCGGTTGACACCATCTTTGTGCTATTGCGGC  
GAAAGTCATGATCCGCTGGAAGCGGCTTATGACCGCCGCTTTGTGCGGGGTGGAATCCCGGCATGCGCGTTCGCTC  
CACCGCAGCTGACAGCGGGCGCACACGCGACTTCTCCGGGTTGACCGGGTATCTC

Clone Rv122

.....:Rv122SP6D2.seq:.....:

GCAGCATGACGGCGGTAGCGAAACACGCGCGGATGCAGCGCAAGTAGCGTCGATGTGCTACGGAATCGCCCCGGGCAAC  
CGGATCTCGRNGATCACGATGCCCCCCCCCTGCAGCGCNAACCCGACGATTCCGTACACCGCCACGCCGATCAGGCC  
TGGCGCATCTGATTGGAGCTGGCGTANATGGCGGCGATGTTGACGATGGCCAGCGCCACATACATTGTGGCGGCCAGA  
ACACCGCGGTTGGGGCGCGGTGCGATGAACACTAGGCGACGCGATGCGCCGGGTCAACAGGTTGACCATCAGAAG  
CTTGCGCATGACACGGCGGCCACTAGGAAGTACAAGAANGTGGCCACACCCCATGCAAGGATCGGGTAAAGGCTGA  
TGGTCCGGAATCGACTCCGCGCTAATACATGACTCTCTCTTTGCGTCATCGCCTTACTTGTGCGCGGAA

Clone Rv

.....:Rv123SP6D2.seq:.....:

GGGACACACCTCGATGCTGCCGCGNATGGAACGCGGTGGAACGCAAGCAGCTGATCGAGTCAACGCCGCGCGGAACGC  
TTCCGCGCGGGCGTGACGCAATCCGTTGACCGCGCGANCTCTCTA

.....:Rv123T7D4.seq:.....:

TGGGCGCTCTTTTGGCGCTTCCCNNTTAAACGNAGCANGACATCTGGGTATCAGATTGTACTGGATGGTGTGGCG  
ATGTCGGTGATCCGTGCTCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCCGGTTGAAAGAGAAATGGG  
GCCGATTAACACCGGAATATTCCTGCGCATGGCTGCTACCGGGGAGTGGTGACGCGCTGCCGCGATGCTGTTGCGC  
GTTACCATGTGCTGTTTGTGTTTCAGCATTTTGGCAATATTGGTCAGATCGGTACCACCATCGCCTTCCC

Clone Rv124

.....:Rv124SP6D2.seq:.....:

CCGATCGCGCGCGCANCTGGTTGGTGTTCGGGATGAATCCGACGCAAAATGATGCTGCGGTGGCGTGTGCTGACTCG  
TNGGCGTCGACGCTCTGTCGACGCCACCGANCGGTTGGTCCAGGATCTGATGGGCAAGTTGTGCGGCCCGCGCGGTG

ACGGCCGATGAGCTGACCGAGGTCGACAGCGCCGTGTGGCTGACTTGGAAACGACATGGAGTCGCCCCGGTTGGCGGT  
CACCTCAAGCATTTTCAATGGTTATGCGACCAAGTTTTTTGGGTACGCCGTGACGACATCACGTCGGAGACTTGGATGAGC  
TGTGTCGCCAGATAGCCCGAATGCGGACGACCGTGGTCACGGTGCCTCTGACCATCGGGTCGGGTGCGCCGCGCT  
ATCGCGATGGTGGCTNATCAAGCGACACGCGCTGCCAAGGANGTNCNGCGGACC

.....:Rv124T7D4.seq:.....  
CGGGTTGGCGATCCAGCGTCGCGGTTGTGACGAGCTACGGCATAACCGCGCCACAGCTCGCCGATCCGCTTTTCG  
GTGGTCTCAGTCACTCGCTGCCGTAGGCGATGCGCAGCGCTGCTCGAATATCGGGTACAGTAGGCGCGCCTTCCNC  
TTTA

Clone Rv126

.....:Rv126SP6.seq:.....  
CTTGATTTTATCATCATGACGATCATCACCTAATTTTGGCTACCCGCACTGGTTATCGTGGGTACCGTCGTGCTTTTC  
CATGGCGCCTCTTTTCGGGCTTTCCGTATTGGCTCGGACGACATTCGTGATATCGATTTCGACTGGATGGTGTGGC  
GATGTCGTGATCTGCTCTGCGCGGTGGGATCGGACTACAATTCGTGCTGATTTCCCGGTTGAAAAAGGAAATTTGG  
GGCGGATTGAACACCGGAATATCCGTGCCATGGCTGGTACCGGGGAGTGGTGACGGCTCGCCGCGATGGTGT

.....:Rv126T7.seq:.....  
GGGGATCCCTAGATGCACTCGAGGATGCAAGCTTGGCGTGTGTTCCAAACCGGAATGGCTTTCCGGCGCATTCGGT  
GAGCGGGACACCTCGATGCTGCCGCGATGGACGCGGTGCAAGCGAAGCAGCTGATCGAGCTACAACGCGCGCGG  
AAGCTTTCGCGCGCGGGCGTGACCGCATCCGTTGACGCGGCGGATCGCGGTGATCGTATGACGGCATCGCCACCG  
GAGCNACTGTCAAGGCGCGTGCCAGGTGCGCCGGGCGACGGTGGCGGACAAGGTGGTGGTGGCGGTCGCCATCGGG  
CAGACGACATCGTGGCGAGATTCGCGGGTACGCGGATGAGGTGGTGTGTTGGCGACGCGCGGCTGTTCTTCGCGG  
NCGGGCANGGTTACCGCAACTTCAACCAGACCTCCGACGACGAGGTGGTGGCGTCTCGTGGATCGTGCTC

Clone Rv127

.....:Rv127SP6.seq:.....  
AAGGTCGAGTCAAGCGGNTGGTTACGACTCCCTGTGTGATGAGCAGCTTCTACTATCTCGCTCTACGCGCCC  
TTGGTCCGCTGCCACGCGGACCGAGCGGCTGCAACTGGCGCGTGGTGACCGGCAATACCTACCGACGCGCGACC  
CTGCTGGCAAGATNATCACACGCTCGACGTGGTTAGCGCGGTGAGCGATCTCGGCAATTGAGACGCGCGGGTTT  
GAATGGAACACCGCAGCTCGGCTTCGAGTCCGGCACTTCAGTGACCGGTTCAACCGGCTCGA

.....:Rv127T7.seq:.....  
CTTTCGCGGTACCGCTCAACTTTGTGTCGACCTCAACGCCATTGCGGCGACCTACTACGTGCACTCCAACACTT  
CATCTGACGCGCGGAACAAATTGACGCGCGGTTCCGCTGACCAATACGGTCGGTCCCAGCATGACCCAGTACTACAT  
CATTCGACGGAAGAACTGCGGCTGCTACAGCACTGCGATCGGTGCCGATCGTGGGAGCCCATGCGGCAACCTGGT  
TCAACCAACTTGAAGGTGATTGTAACTGGGCTACGCGACCGCGGCTATGGTTATTGCACTCGCCGNCNAATGT  
TGGCATCCGTTGGTTCAGANGTCAGCCGGTCTCATGCGGACGCTCTGCTCN

Clone Rv128

.....:Rv128SP6.seq:.....  
CGGTATAGCCCTCGGGTCCGGCCAGCACTCCGAGGCTTCGTGGGGTGGTCGCGACGCGCATGGGCCACCATCGCA  
TTCACGAGTCTGCGGAATCACCAGCAGTAGACGGTTCCTTCTTAAGCAACACCGAAGTTTACGACCCGAATGC  
TCCGGGAAACATGTACGGTAGGTTCGGTATTCGGCTACCGGCTGAGCATTGAGCACGCCGGCCAGCACCGCAGCAGC  
CAGGCAATCAGCGCGCGCGCACCGATCGCGGTGACCACTGAGTCTCCGGAGACAATGCGGCGCGCACGCGGNCCTC  
CGCGCGCACCGCTACNCGCCCGGTG

.....:Rv128T7.seq:.....  
GTGATGGACAGCCACCGGACACACCGCGCTGCGCTACNTAGGCAATACCGGGCGGAGCTACATCGGCTCGGCGCG  
CCAGTCTCGGGCCCTCTTCGAGGTGAGGTTCGATACCGATTGCGCATCCGCAACCGCNCCTGGACGACAGAACC  
TGTCCTACGATGCTTTGCGGGCGGGCCAAAGAACAGTTGGCATCTTCGCGCGGATGGCGCGCGCGGCTGTGTC  
GCCAAGGACGACGCGGTTCCGGTGTGATCGACGACGCGTGGGTTTACCGATCCGAGCGCACTACAAGATGGGG  
AGGTCTCTGACACCATCGGCCCNACGGACATGTGATCGTGCGGACGTGACGTGCCACCCG

Clone Rv129

.....:Rv129SP6.seq:.....  
GCGAAAGTCGTTGGTGCATGATGTAGCGCTTCTCCCATCGAGATAGTGGAGCAACGCAATCCGTGCGGTACGGT  
TCGGGTCTGACTCGATGTGCGCGACCTTGGCGTTGACACCATCTTTGTCATTGCGGCGAAAGTCGATCATCCGGTNNG

CGCGCTTATGACCGCCGCTTTGTGCGGGTGGTAATCCGGCCATGCGCGTTGCGTCCACGCGACCGTGCACGCGGC  
GCACCAGCGACTTCTCGGGGTGACCGGGTGATCTCGCGAAATCAGATACGCTGGCGCGGACGACGAGCGTCTG  
TGGGCTTTGCTTCCGAATGNCATGTCTAATCANGTCTTTCTCTCAGCGTCTCGTGCGCCGGGTAGGCCGCATTCGC  
CTGCTCTCTCTGCTGCGTTGCGTGTGATCGTCCCCGGGCTAAGCCGTCGCCCGAAA

::::::::::Rv129T7.seq::::::::::

GATGGTTCGGCGCACGGTCAACTGCCACACGGCACTGGTAAGACTGCCCGCGTTCGCGGTATTTCGCGGTGGTGAAAA  
GGCCGATGCTGCCGTTGCGCGGGGGCGGATGTTGTGCGGAGTGACGATCTGATCGAGAGATTTCAGGGCGGCTGGCT  
GGAATTTCGATGCCGCGATCGCGAACACCGGATCAGAATGGCCAAAGTCGTCGCATCGCTCGGGTGCTGGGTCCGCGC  
GGCTGATGCCAACCGAAAACCGGACCGTCAACCGCGACTCCCATGCGCGTCCCGGATATCAAGGGCCGGCAAAAT  
CAACTTCCCGGTTGATCAGCAAGGCAACCTGCCCTCNCNCTCCGG

Clone Rv130

::::::::::Rv130SP6.seq::::::::::

ATACTCAAGCTTCGTATAAGACATGGTGGCTTTCTTTACCCGTCAGAGTCGGGGGCATCCGACCCGGCTCGCA  
TCGGATCATCTCTCCACGACGCGGCGCTCATCAGCTTGGCCATTTCAATCTACTTGATACCCCGCGCTGGCGGTAGG  
CCACTGCGACAAATTCAAAACCGGTGTACACGGTGAATAGTGTCCAGATGGGCTCTGATCAACCGTCGCAAAACCGGT  
TTCCGATCAATAGCGAAATCCACCGGGTGTGATGGAGGCTGTGACTTGGAAAAAATAATTTTTCATTACAAACA  
AACAACCGCCNCGAAACTTTGCA

::::::::::Rv130T7.seq::::::::::

CGAATTCGGCGTGACCGCTATGGGTTGCAGCAGCGCGTGGCGCCGACACCCCACTGGCCGGGTGTTTTCGCCCCG  
AACCAGGATCATGTTGAGCGAAAAAGGATTCGCTGTTCGATGCTGGGATTCGCCACCGCGAGGGCCATCGACCGATT  
ACTCGCCACCGGGTGCAGAGGTCGCCAGTCCCGCTCCGTGCAGCTTCCGACGATCCATCCGGCTTCGCGCGTCG  
GGTGGCGGTAGCCGTCGATGAAATCGTTCGCCGCGCTACCTGCAAGTGATTCTGTCGCCGTTGTGTCGAAGTGCTT  
TCGCGATCGACTTTTCGTTGACCTACCGGCTGGGGCTCGCGACACACCCCGGTGAGGTGCTTTTGTTCAGTTGG  
CGGAATCGTGCTCTGGGTTACAGCCCGAACTCGTCACGCGGTGCGCGCCGACGGAGTTGTTATCACCAGTCCGT  
TGGCCGTACCGCGCCTTGGG

Clone Rv132

::::::::::Rv132SP6.seq::::::::::

TCAGACTCCACCAGCCAGCGAGGACGCGGAAGCTGAATCCTCCAACCGGGTTGCGATCCGGACAGGTTGGGGTGCG  
TTTGGGCAATGACAGGTGGCGCGGTGCGTTTCGGGTGCGCGCGCGGAGGTGCTGCTTGGGATCGCCCGGCTGGGCA  
TTTCNGCGTGTGGCGCGCGCGGTGCTGGGGGGCAACAGGTGTCCGCGGTGCGCGGTGGCGCTGCAGCGGTGCAGCGG  
GGCGAAGCGGTAACCTTGGGTACCGGGGCGCTGCTCGGATCGCGTGGCGGTGGCGGTCGCGGACCGCAACGCTGACC  
AAGCTGCGGCTGGCATTCGCCGCGATAGCCAGTGGCGGCAATGCTGCTTTCGAGAGTGTCAAGTGGGGTCCACCTGA  
TGCATGGCCAAAGAACCTACCGTGTAAACGNCACACAGGACCGCGCGGTCGCT

::::::::::Rv132T7.seq::::::::::

TTTCCGGGTACCGGCTCAACTTTGTGTTCNACCTCAACGCCATTCGCCGCGACCTACTACGTNCACTCCAACCTACTTC  
ATCTCGACGCGGAACAAATTCAGCAGCGGGTCCGCTGAACAAATTCGGTCCGTCCCAACGAAAGAACAGTTTTCNCT  
CTTTTCNACGGAGAACCTGCCGCTCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCACTGGCGAACCTGTG  
TTTCAACCAACTTAGAGTGAATTTGAACCTGGGCTAGGGGAAACCGGCTCTAGTTTTCACCNCTCTCGGCCCG  
NTGTTTCGAAATACCTTCGGTTTCGGGTTGCCCAAA

Clone Rv134

::::::::::Rv134SP6.seq::::::::::

GCTTCGGGTCGTATGTTGTGGAAATGTGACCGGATACCAATTCACACAGGAAACAGCTATGACCATGATTACGC  
CAAGCTAGTTAGGTGACGATGACACTACAACTCAAGCTTCGGGCTGGTGGGCGGACCACTTCGATGGCAGCAGCCGTA  
ACTGCTGCCCGGCAATTTCTTGGTGCGCCGGACCGATGGACCGCGGTGGGATTCCAGAAAGTGGCCGATCCCGC  
CCTTGGGAAAAACCGGTCACCTCTACTTCACGACCAACGAC

::::::::::Rv134T7.seq::::::::::

CCGATCGACTGATCGCCGACAAACAGCGCCCAACCACTGGAATGAACCGTCGTGACCATCATCAGCAGCGGTTGTA  
GGGACTTTCGACATGTTCAACCCCGGTACTCGGACGGAATCTTCAACCGAAACAGCCAGCTCGGCCAGGCTTT  
CACGTACTGCTGGGGATCTGGGCAACAGCTCGAGGACGCTGGCTCCAGCGGTGTCTAGGAATTCGCCAGTTTGAC  
CAGAAAGCCTCGGTTCGGGCTCTCTCGCGTCCGACGGCTGGGAAATGGGTGATGAGCCTACGGGAAACCGGCC  
CACAAGAGGTTCTTGGCGAAGGACGGTTTATCCAAACCACTTCGCGAGATCTTCGCAAGGGGCGCGCTTGCTC  
CTCGGTGACTGAGTTGTGCTGTCATCGCGCCTCTCCTCTGA

## Clone Rv135

:::Rv135SP6.seq::::

TGCATCCGGCTCGTATGTTGTGGAATTTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG  
CCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTTTACGGTGATCGCGCATCACTGGTTTCATGAACCTGGAAGC  
AGCGCAGCGCTCCCTTTTCGGCGCAGCAATGAGCCAGCCTCTCGTCCGGCGGTGGGTGCAGGTGCTCGGGCAGCTCGG  
CGCGCAGCGCGCTGACCTGAAACACAGCTTCCATATCCCGCAGCAAGCAGCGCATCCGCTACGTAACCCCTCCG  
GTCACTGTCATGGACAACAGCGCTTCTCCACCAGCCGGGCCGGGTGTGGGGTGTTCGGCGACCGGACGCCAGCTG  
GTCCACTGCTCCGACGGCGCCGAGCGCTTACCCAGCAGCGCCGCGAGCAAGTCCGCCGATCGCATACTCC

:::Rv135T7.seq::::

GGGGCGCTGCTGGTATAGTCGCTGACCAGGTTCGACAATGTGGTCCGGTTCGGCGGCTAGCTGCCATCGA  
GACACTGCGAGCGCTATCGCACCCGTTATCGGCTACGAGCAAAATCGCGGTATGCGTTCTTGAGCATGAGTCGCGGAC  
CGTCGTGATGGTCGACACCCAGCAGCGAAGACGCGATCGCCGTCAAGCATGTGTGCCCGCGGATTATCAGGACTGAC  
CTCTGGCTGAGCAGCGCATGTTTGGTCGCGATGCTTGGCGCCCGCGCGGTGCTGTGGTTCGGCTCGGATAGCGAGGT  
CAGCGAATTTCTCGTGGCAGCTCGAAAGGGTCTGCGCGGTGCCGCTTTTGGCGAAACGATGGCGCAGGTACCGGTGCG  
CGGGGTTCGGGCTGCGCGGCCAGACAGAGTTTACCGATGCGCAGCTAGTGGCGACAGGCTCAGCCAACT

## Clone Rv136

:::Rv136SP6.seq::::

TGCTTCGGCTCGTATGTTGTGGAATTTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG  
CCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTCCGTACAGGTGCGCTTCAACACCGCGGGGAGCGACACCA  
GCTTACCGAGCTTGGAGTCCAGGACCCAGCGCGCGCTCGGTCTGCGTGTGGTGGCGCGGGGTGGCTTGGCTGG  
CAACGATCTCCACCCAGCGGTGCGGTTACCCACGATCTCGCATAGACGCGGGCCGAGGCGGTCGATACCGTATT  
GCGTCAATTGGGACGCGGTTGTGCATTGCGCTAGCTCGGTTGCCACACCGCTAGGGGTTGACGTTGCGGGTTCGG  
CGGGCCCGACACCGCTGTACCATGCCCGCAGGCCGACCTGCGGCGCCACCACT

:::Rv136T7.seq::::

CGGCATGACCAACCGACAGGCCGACTGCTGATACCACTCGAAGCGCGGGGTGTTGATGTCCGACGCGTGAAGTCGTC  
CTCGCGCGCAGGCGCTGAGCAGGTACAGGCGCGCGGAGTTGGACCAACCACTTTGGAATTGGACCTTGATGTACG  
GCCATTCGACGGCGAGCGGACCTCGAGTACTCCACGCGCAAGCCGCGGCGGAAATGCCCCCGGCTCGCGCTGCC  
ACCGACGCGGCGGACAGCAGACCTAGAGGCGCGCGGACGCGGCCGACACGATGACGCGACATCCCGTGAC  
GGCGCCACGACCTGTCAACAAGCTGCATTCTGCTTCCCTCTCTCATCTCAACGCATCGATCGATTTTGGGCG  
CATCTGAATTANGTCAGACTGCAGGCGCTGGCGCGGAGTGTCTGTATCAACCAACTTTCGGGGT

## Clone Rv137

:::Rv137SP6.seq::::

TTCCACCCATAATTGGCTTTCGGGCCCATCCGTGAGGACGGGTGCGGGTCTCAACAAACAGCTGCTCCGCGGGACA  
CACTCTATGCTCGCGCATGGACCGGTCAGCTGACGAGTCAACCCCGCGGGAACGCTTCCGCG  
CGGGGCGGTGACCGCATCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACCGCATCGCCACCGGAGCAGCGCC  
AAGGGCGGTGCCACGTGCCCGGGCGGACGCTGCGGACAAGGTGCTGTGGCGGTCGCCATCGCCCAACGACATC  
GTGGCGAGATTCCGCGGTGACCGCGATGAGGTGTGTGTCTGGCGACCGCGCGTGTGTTCTCGCCCTCGGCGAGGGT  
TACCGCAACTTCAC

:::Rv137T7.seq::::

CAGGCTCAAGCTTTTCGGCGGATACCGGCATGTCCGCGCATCCAGGACTTCTGGGGGATCCGCTGACAGCGGG  
GGATCCAAAGTGGGATGATCGGGCGGCTACGTCGTGGTGTACCTCGCGGTAAACAAAGAAACGAGCGTATGAC  
TCGGTCCAGCGGTGCGGCGCATGGTGGACACCAACCGCCACCGCGGGTGAAGGCTTATCGACCGGTCCGCGA  
GCATCAATGCGGACGAGCGCGAGGCGGAGACAAAGATGCTGCTACCGCGTACCGCGGATGATCTGACGCGTCCGCG  
AGCAATGTTGCTAGTGATCTATCGCTCCGTAATTAACGCGGTTCTCGTCTTATCATGCTGCGCATCGACTCGCGCAA  
TCCGCGGATTCATCGCTTGTCTCGCGAACACAACATTTTACCTTTTACATTTGACCAACCTGCTCTTCTCAT

## Clone Rv138

:::Rv138SP6.seq::::

CATCTACTCAGCTCTCTCTCATTTACCACCCCTGTAATTTGGGATGGGCAAAAAGCGAAGCAGCGCTTGGCCACNA  
CGCCCGGAGGAGCAATCTCGGGCGGTATGGCTTCTCCGGGAAGGCCCAACGTAACGGCTTCAACACGTCGCGTC  
GCCCTCCGAGCGAATCATTTGGGGATTTGGACCAACCTGNTACCACTCGCTGCGCGGCGATGATCTGACGCGTCCGCG  
CGGGTAGTCCCCGCCGGGCGGCTACGCTGAAACCCGATGACCATCGATGTGGTATGAGCATCCGACGCAAGC  
GTTCTCAACGCGCGGATGTTGTTCTCTCGCTGCGCGGTTGACCGGTGGGTCTATCCCTGAACCGCATGCTCCN



CAGGCATGCAAGCTTGCTGCATCTTCCGTGACTGCTCCGAAACCTGGGGGTGCGCTGCTGTATGCACGGCATA  
 CGGCATCATCTTCCCCTGATACCCGGCGGTGCAACAGCAGCTGTTCATCATCAGGGGTCAACCCGGGCAAGGGCGAC  
 GCGACGCCAAGTTGGTCCCGCTTAACATGCTGTGATCTATTGCTGCGAGCAAAACGCTGCTGCCCGTTA  
 GGAAGTGAATTGAAACTCAACCGATTGGTGCCGCGCTAAGTGTCTGCTGTGCGGGTGCCTGTGTGTCTCCGCGGT  
 GTTATACAGACAAATGTGACCGGGGAGGTGCAACCACTGGCAGGCGTCCCGGAAAGTCCATTGCGGGGGAAGAG  
 ACAC

## Clone Rv142

:Rv142IS1081.seq.:.....

GAAATGCCCAAGGTGTTGGTGAAACTCGCTGGACGGTCCCAAGGATGTGGCAGCACATTACC CGGACATGACCCG  
AGCAAGACCGGACATCTCCCATACCGTGTGCGCGGTGTACATCCGTAGCCCGTCTGGCAGGTGCTGGGTGAACAA  
AATCAGCCCAACACCTGCCACGACGAGAAGCGGGTTCGGCTGGCATGTCTTGTGGCTCGCGCATGCAATTCTACGA  
ATTCTCTTATCTAGCGGACCGCTGCGCGCTGTGTGTTCCACCGCTGTTCTCCCAACCTGGATCCACCGGTGGCCG  
CGTGGCTCCAGGGGACATTGCTGTGGCTTCTATCCCGGCGTTCGGCGCGGCGCTCTTTGGATACTTTGGAGA  
CGGCTCGCGCGCCAGAACCTGGTCCGACACTGTTGATCATGGGCTGGCAACCTGACTGTTGGGCTGGTTCC  
ACGACAGTGGCCATCGCGC

:Rv142SP6.seq.:.....

ATATTCAAGCTTTGTACACCAAGTGTCCGACCAANCGTCCATCCGGCGAGTGGATACTCCGACAGGTAGCAGGT  
CGCCACCAACGCTGGTCAGTGCCTGTCATCTCGCTTGGCGGCTGCAGCAGCCAGTCCGGAAATAGTGCCTGGCG  
CAGCTTGGGATCGCAGCTCGATGGTTGCGGACGGGTGCGAAATCAGGTGGCGGTAGCCGTTGGCTGATTGGA  
CCGCTCATCGCTGCGTTCGCGGTAGCCNCCCACAGGCGCTCGGCTTACGCCCATCCAAAGCGCGCGATGAACG  
TCGAGAGCAGCCGCGCAGCAATCCGGGCTCGCTGCGAGTTGGTCAGCCAGAAGCTGCTCGGTGCATAAGATG  
AGAAGAGTCAAGTGCCTCTTCTCTCG

:Rv142T7.seq.:.....

CAGGCATGCAAGCTTTTGAGCGCTCTCGCGGGCAGCTTCGCGGCAATTCTACTAGCGAGAAGTCTGGCCGATACG  
GATCTGACCGAAGTCGCTGGGTGCAGCCCAACCTCATTGGCGATGGCGCCGACGATGGCGCTGGACCGATCTTGTG  
CGGCTTGGCCAGCGGACGCGGTAGTGGTCAAGTCCGCTTACGCTTGGGCTTTGGGACGCTCCGACGCTGGTC  
CGGTTGGCGCGCCGAAAGCGGGTGGGTGGCATCATGAATGCTCACCGCGCGCGACTGCACGCCAGTGGCCCG  
GGCGATGTCAGGCATCGGACATCATGCTCGCTTCTACTCTCGACCAAGTCCCGGGAACAGCTCCATTCCGGAAC  
GCCAACGC

## Clone Rv143

:Rv143SP6.seq.:.....

ATACTCAAGCTTTTGGCTGGTCCGCTTCCAATTCAAGCTGCACCGCTATGGGTTGCAGCAGCGGCTGGCCCGCACA  
CCCCACTGGCCCGGGTGTGTTTCGCGCGAACCAGGATCATGGTGAGCGAAGAGGATTNCCTGTCGATGCTGGGA  
TTGCGCACCGCGAGGCCATCGAACGATTACTCGCCACCGGGTGGGAGAGGTCCGCGAGTCCCGCTCCGTCGACGCTC  
CGACGATCCATCGGCTTCGCGCTCGGGTGGCGGTAGCCGTCGATGAAATCGCTGCCCGCGTACCACAAAGGTGA  
TTCTGTCCGCTGTGTCCAAGTGCTTTTCGGGATCGACTTCCGTTGACCTACCGGCTGGGCGCTGGCACAACACC  
CGCTGAGTCTGTTTTGTTGAGTTGGGCGGAATCCGTGCTGGGTTACAGCCCGAAGTCTGACGGCGGTGGCGC  
GCCGAC

:Rv143T7.seq.:.....

CAGGCATGCAAGCTTCAACCTATTGACGCAATTGTGCGAATGACGGCGCCCGCGCATGGCCATCCGGGAAGACCATCA  
TTGGCCAGTGGCGGGCGGTAAACAGTTCCAGCCCCACAGTGCCGCTCGAAATCGGGTGAACCCATTCGAGAG  
CGCGCAGGGAAGCCAGCGGGAAGCGCAAGGGCTGCAAGTCCGCGCCCAATAGTGTGCTCGCAACAGATGGGCT  
CGAATAACCGCGCGCGCAGCACCAGCCGACGCGAGGTGAGAGACGTCGTGACGGCGCCACATGGGTGCCAAT  
CGGCGCGGAGGTAGCCGCGCGCAACCCCAACGCGTGTGATGCACGGTCCGAGGAGGCCACCAACC

## Clone Rv144

:Rv144SP6.seq.:.....

ATACTCAAGCTTCCGGCGCGAGTGACGGCGGGCTAGCGCCACTGATGCCGACCCGATCGACGNCGTGGTTC  
GGGTTGACTGGCCCGCGCGGACGAGGCGCTCAACCGCGCCCGGACGTCGGCGGCGCTCACCGCTCGGCATTCGCC  
CGGCGGGAGTCTCGCTGAGCTGACCAAGTAGACAAGTCCGCGCTGGCGCTCGAAGACAACGCTGTGCGGTGTGACG  
CGGCGTAGAGGCGCGGCGAGCTCTCGGTTTCGTCGTAGAGATACGGGAACGTCAGCGCTGGCGCGCGGCTCGCG  
GACCATCTGATCGGCGCGCTCTCGGCGGTAGGTGACCAAGTCTTACTGGAGATACGACCATCGCGGACCTTTGATC  
GGCGAGTCCGCGCGACGCTGGCCAAATCCGCGCGGACGCTGTCGCCGTACCGGCGAGTGGTTC

:Rv144T7.seq.:.....

CAGGCATGCAAGCTTTANCAATCAACCCCGCCCGCAGCACCGACAGATGTCGATGCCATCGAGTGAATGT  
CGAATGCGCNAACCATCTGGCGACCGCGACACCGGCAACATGGTACCGCGATTTCGGTGGCAATGCCAGCC  
GACGGCGCGCTCTCACCGCAGGTGACCTCGATCAGGACAGCCGCGCGTATTACTCAGCACCCCTACCGTGTCA  
CGCCCAAAACGGCGCTGGTGTGATTTCCGGAGTGACCCGCAACCGAGTGTGCTGCCCGGATCCGCGACCAATCC  
CGACCCCACTCGCCAAACCGGAATCAGCGTGTGCGCTGGTAATGACACCGACAGTAACGTCATACGCGCCGC  
ACCGCGAGCCGCAACACCGACATGATGATCGGCTG

Clone Rv145

```

.....
:::Rv145SP6.seq:::

```

ATATTCAACTCTGCACACTTGACGATACCTTGGTCAGGAGACCCAAAGCTGGCCTCCACCGCGCGCGGGGACCA  
CGGTCATACCTTTGANNCGCTTTCCGATCGTTGATCGTCGCTGCGCGGAAACCCGACGGCTGGCATATGACGAGT  
GGGCGCATCTGGGCACTTCGACATCCACCGATTTCGCCCGCATACAGCTTTCAGCGCTCCCAAGTTGATCATCGACG  
GGCTGCCGGATATCCCGCACTTTCGGCTGGCGGGTCAACGGCGCCCGCTTCGGACTGAACCGCGCGTGTTCGTCGAGG  
ACCAACGAC

.....Rv145T7.seq.....

CAGGCATGCAAGCTTCATGCCGCGGCATGATAGCCACATGCACGCAATCGAACTCAGCGAAACCGGCGGGCCAGGCG  
TCTTACGCCACCTCACCAGCGCGCAACCTCAACCCGGCCACGGAGACCTCCTGATC

Clone Rv146

```

.....Rv146SP6.seq.....

```

ATATCTCAAGCTTGATTTTGATCATCATGATGATCATCACCGGAATTGTTGGTAGCCGCGATGGTTCGTGGGTACCGT  
CGTGCTTTCCATGGGCGCCTCTTTCCGGCGTTTCCGTATTTGGTCTGGCAGGACATCTCGGGATCGAGTGTACTCTGGAT  
GCTGTGTGGCATCTGCGGTGATCTCGTCNTGGGCGTGGGATCCGATACAAATTCTGCTGGTATTTCCGGGTTGAAAG  
GAAATTTGGGGCGCGATGATGAACACCGGAATATTCCGTCCATGGCTGGTATACCGGGAGAGTGGTGACGGCTCGCCGAT  
GGTGTTCCGGCTTACCAATGCTGTTGTTGTGTGTCGAGCATTTGCAAAATTGTTGGTCAGATCGGTACCAACATCGGCCT  
GGGCTTGCTGTTCGACACCCCTGTCGTGGCCTCTGTCATGAACACCGTCCATTGCTGCCCTGCTGGGACCTGGTCTGTGT  
GGCCGCTACGGGTGGCCGCGCGCCCGGACGTCFAAATCTTCCGCGC

```

.....Rv146T7.seq.....

```

CAGGATATGCAAGCTTGGCGGCGCTTCAACCCGAAATTGGCTTTGGCGGCGCATCGGTGAGGACGGCGTGC GGGGTCTCT  
 AACACGACGCGCTCTGCTCCGCGGGACACACTCATGTGCTGCCCATGACCGCGTTCGAACGCAAGCAGCTGATCGAGCTAT  
 CAACGCGGCGCGCTGCTCTCCGCGGGGGCTGACCGCATCCGCTTGACCGGGCGATTCGCGGTGATCTGTCATGAC  
 GGCCATCGCCACGGAGACGGCCAAAGCGGCGCTGCCAAGTTCGCGCGGCGCACAGTTCGCGGACACAGTGGTCTGGCG  
 CTGCCATCGGCGCAGACGACATCGTGGCGAGA

Clone Rv147

```

:Rv147SP6.seq:

```

ATATCTCAAGCTTTTACGGTGATCGCGCATCACTGGTTCATGAAGTGAAGCAGCGCAGCGCTTCTTTTCGGCCGC  
ACATGAGCCAGCTCTCTGTCGGCGGTTCGGGTGCAAGTGCTCGGACAGCTCGGCGCGCAGCAGCGCTTGAACCTGA  
CAGCTTCCATATCCCAGCGAGCAACGACGCCAGTCCGCTACGTACCTCCGCGAGCTGTCATGGCAACGACGCGTT  
TCCACGACACCGGCGGGGTGTGGGGTGTTCGGCGACCGGCAAGCCCTGGTGTCCACATTCGCCGAAG

.....Rv147T7.seq.....

TAGTCGCTGACCGGTGCAGGTTTCGACNATGTGGTGCCGGTTCGGCGGCTACGTGCCATCGAGACACTGGCGCAGGCT  
ATCGCACCGGTATATCGGCTACGAGCAAAATCGCGGTATGCGTTCTTGAGCATGAGTCGGCGACCGTCGTCATGGTCGAC  
ACCCACGACGGAAGACGCGAGATCGCCGCTTACNCNTGTGTGCCGGCGATTATCAGGACTGACCTCCTGGTGACCGGC  
ATGTTTGGTCGCGATGCCTGCCGCCGCCGCGCGGCTGGTCGTGGTCGCGCTCGG

Clone Rv148

```

.....Rv148SP6.seq:.....

```

ATACTCAAGCTTTTCGCGCGTACCCGCCATCTCGCGGCATCATCGAACTTTCTGGGGGGATCCGCTGACAGCGGGCGGA  
TCCCAAAATCGCGGATGATCGCGCGCCCTACGTCGTGGTACCTCGTCGGTAAACAAGAAACGGAAGCGTATGACTCT  
GTCCACGCGGTTCGGCCACATGGTGGACACACACGACGACGCGGGGTGAAGGCTATGTCACGGTTCGCGCAGCA  
CTCAATTCGGCATGACGCGCGGCGGAGCAAAAAGTATCGTAAAGTCACCGGATACACAGGATGGTATCGCAGCA  
ATGTTGCGTAGTATGCTCGCCCTTAATTCACGCGGTTTCGTCCTTATCATGGTCGCGATGCACTCGGCGCAATC  
CGCGAATTCNTCGCCTTGTCTGCGCGACCAACAACATTTTCAGCCTTTCAACATTTGCGACAACCTGCTCTTCTCATGG  
CGATTGCGGCGAAT

.....Rv148T7.seq.....

CAGGATGCAAGCTTGGCGTCCGCTTCCAACCCGAATTGGCTTTCGGGCCCATCGTGAGGACGCGCTGCGGGTGCTC  
AACGACGACGCTGCTGCTGGACACGCTCATGATGCTTCCGCCATGACGCGGTGCAGAACGACAGCTCATCGATGATC  
CAACGCGCGCGGGAACCGTTCCGCGCGGGCTGACCCATCCGTTGACGCGGCGCATCGCGTGCATGCTGACGTAC  
GGCATCGCCACCGGACGACGCGCCAGGCGGCGTGCCAGTGCTGCCCGGCGCACGGTGGGACAAGTGGTGCTGGCG  
TCCCGATCGGCCACAGCAGACATCGTGGCGAGATTCCCGGGTACGCCGATGAGTGGTGTGTTGGCGACCCGGCG  
TTGTT

## Clone Rv149

:::Rv149SP6.seq:::

ATACTCAAGCTTTGGCATTTGTGCACATTTTCCACCCGGTGCCTATTAACTGCTGAGCCGCTAATTGTGACCCCACTCGG  
GAAACACCGGGAGCACAATAATTCACGCGACGGCCGGGGCGGTTCAACTCACCATTGGATCGCTCTCGTCTGTTGGTGC  
TGGACAATCGTCGCTGTAGCGCGCTCGCGAACACCTCAGCTTCTGCTGCCCGGGCTTCTTCCGGCGATGGTAACCCCA  
GGTTTCCGCCACGGTCTTACCTAGTAGCGGACGCGGTGTTCACTCTGCATCGACCTGTTGACTCATCTGTCAAGGAT  
GAAGGCGTACTGGGCGGACTGCGCCTTCTGCCGCGCCAGGTGCGCAATCACCAGGATCTCAGAAACGAGCTGCGGACTC  
ACTCTTCCAGGCGACCTTGGCCGAAAGCTCGACATGGTCAATCCGGCCG

:::Rv149T7.seq:::

CAGGCATGCAAGCTTGGCGGCCGAGTGGTTTTCGACGGCCGCTCGCTTCTCGGCATCGGTTTGGGCTGTCAACGAGAG  
TTGGTAGTTCTTCACTACTGTTGTTTCGAGCGCTCGAGCCGCGCGCGTGTGAGGTGCGCCGGGAGCTTACCCGCCAG  
GCCGCTCAGGGTGCCCTTCCAGTCCACGCCGCTGTGGTTCGCGCAACCGCTTATCTTCAATCAGACGATCCGCGAGCTT  
CATCTGTGTTGGCGATCTTCCGAGGGCACTTCGAACCGGCGCTGCGAGTACAGCCACCGGATCTGTTGTCCTTCGCG  
GTCGACCATCGTCGATACCGCAGGCACTTGCCTTC

## Clone Rv14

:::Rv14SP6.seq:::

ATACTCAAGCTTCCGCGCGGCCAGTACCGAAAGCGCGAACAGCTCGCGGCGAGCCACGACGTGCTGCTCGGATTGCG  
GGCGGCAGAAATCAATTCAGGCAAGCTCCCGGACAAATCGGCTCTGCTGGCCGCAACGAAAGGATCGAGTCAACCGCAG  
GTGCCCGGGGTCTGGTGCACCTGCCGATCGCAGAGTTGGCCCAACACCGCGCGTGTGATGCCCGGTTCGCGAACGCC  
GGCAGTTGCCAAACGAGCTGATCCGCTCGGCTCGCGAGTTCGGCGAAGAGTGGTCCGCTGATCACTACCATC  
GGCCAGGATCTGCGGTGTATCACAAAGCTCGCCACAGGAGGTTGTTGTGGTGTATCGACGGCCTTTAGCCAGATGTTT  
GGAATCGACTATCCGATGTTGTCGCGCCAATGGACTTGATCGCCG

:::Rv14T7.seq:::

AGCTTCGGTGTAGCCGATACCCGGAAGCGCATGATCAGCCAGCTTTTCGCGCCGCCCGGCATACGGCGGCGTACCGAT  
CTCCGCGTCATACACCCCGGGTAATCGCCGACGGTCCCGTTTCGCGAGCCGAAGGTGACGACGCTGATTGAATCGAG  
TTCAGAGTTCAGCGGTTGGCGCAGCAGCGCGGCGAGCTCAACGAGCTCAATCAGTTGCTCGCTTCTACGCTCACCAG  
CCCGGTGACCGTAGTCGCGCGGTGCGCTCGGCCGAGAAGTTGCACCGCCACACCGCGACACCGCTTTCACCGCGGAC  
GCCACCCCGGATCGGTTGTGCCCAAGGTAATTTGGTCTATTCCATTTGACGGGACGCCGACCCGCGCCAGTAC  
CGCCACGACCAACCGCGCTGACCCACCACTGTACGAACCAACGAGGCGAGCCGGA

## Clone Rv15

:::Rv15SP6.seq:::

ATACTCAAGCTTCGGTGGCTTCGCGCCGCTGCGCGGTTGGACTTCATGACAACGCGGGGCGATTACCCCGCTACCG  
CAGCAGCATGACGGCGGTACTTAACACCGCCCGGATGCTCGACGCTGCTCGATGTGCTCAGGGAATCGCCCGCGG  
ACCGCATCTCGAGGATCAGCAGCTTATCCCGCGCAGCGCACACCGAATTCCTACACCGCCACCGCGATCCGCG  
CCTCGGGCAGCTGATTGGAGCTGGCG

:::Rv15T7.seq:::

CAGGCATGCAAGCTTCCACATGTACCGATCCACGAACCTCCGTTGAAGTACAGGTTGCGGCCGCGCTCGATCAGGCC  
GGCCACTTGTCTACGCGGTTACCGAAGATCTCTTCGCTGACCTGCCCGCCGCGGCGAGCTCGGCCAGTGGCCCGG  
GTTGGCCGCCGCGGCGACGATCTTGGCGTCCACGGTGGTCCGGGTTCTTCCCGCTAGCAGATCCGCGAGTGGCCGG  
TACCCCGGCT

## Clone Rv151

:::Rv151SP6.seq:::

ATACTCAAGCTTTCCAAGTCCCAAGTGTGATGCTGCGCAAAAGGCTCGACAAAGCGGTAGAGGCGTTTCGGACCCGC  
CGGCTCGATGCCGCGCCGTATACCTTCTCGCCGCCGACGCCCTGTTGCTCAAGTGGCGGAGGAGGCCGCGTCTGTC  
GGGGTGACACCTTGATCGCCACCGCGCTCAACGCCAGGGCTACCGAAAGATCTGGGATCCAGGTCACCTCCGCG  
GAAGACGGGGCGGCTGGCTGGCTTCTTCCGCGACTGGTCCGCCGCGGCTGTCCGGGTCGCGCTGGTCAACAGC  
GACGCCACGCGCGGCTGGTGGCGCGATCGGGGCCACCTGCCCGACGCGCTGGCAGCGCT

:::Rv151T7.seq:::

CAGGCATGCAAGCTTCAACAGTAGGCGCGCTCGATAAATGACTCCGCCGCGCTTCGCACATCTCGTAGCGATCCTTG  
CGGACAGGTCACCGCGCGCTGCCGCTCGAGGAGCGGTTTTTGGCGTGCAGCAGCTGGCCGACACCTCGGGGGGTA  
AGCGAATGACGAGCAGGAGGACGAGTACGAAGCTCGCCAGCTGCGCCAGCTCAGGCGGATGTGCGCGGCT  
CGCCACCGCGTACCCCGCATCGGACCACTGTATGACCGCGGCGACGTC

## Clone Rv152

.....:Rv152SP6.seq:.....:  
CGCGGGCGCGCATTACCCCGCTACCGTCAGCAGCTTGACGCGGTAGCGAACACCGCCGGATGCAGCGCAGGTGCGGT  
CTATGTGCACACGGAATCGCCCCGGCACCGCGATCTCGAGGATCACCAGTGCCTCCCGCTTC

## .....:Rv152T7.seq:.....:

GGGATCGAGGAACAGCGGTTGAACCTGATAGGTGCGGCGCGGTGAGCAGCGCCGGCATTTGTCGATGCGGTTACC  
GAAGATCTCTTCGGTGACTTGCACCGCGCGCGGACGATCGGCCAGTGCCTCGCGGTGGCGCGCGCGGACGATCTT  
GGCGTCCACGGTGGTGGGGTCATGCCCGCAGCAGGATCGCGCAGCGCGCGGTGAGCCGGGTGAACCTTCGTCGAGAG  
CTTGACCTGCGCTCGGGGAGCGAACACCGGTGCGTGCGTATCTCGACACGCGCGCGGCACTCGGGGGTGGCGCC  
GACGGTGAACAGGTTGCGCTGCCACCGCGGGTAGCGCGCGGCACTATGCCGATGCCAGCGCGCGGATCACCAGGTGC  
GGTCAGTCGGGTGAGGATGTCGCCCGCGCCAGTCAAGATCCAGCGGGCGCGCGCGCGGTGGACACNGGTGATCTC  
GTCCACCATCGACTTTCTGATCA

## Clone Rv153

.....:Rv153SP6.seq:.....:

TAACCTAAGGCTTGCCTTAGGCCCCAGGCCCATCGACGGTTTGGCGGCTTAAATGCATGAGGTGCTCAATTGACC  
CCACAGCGGAAATGCGCATCTTCGACGGCTCTCTTCGCTTGGCTGCGGAGAGGGGCTCCGCGGGAACCGCATGCA  
GGTATATGACCTCGGTTTCTCGGGTCTACCGCGTGCTTTCGAGGATGAATCTCGCGTGGAAATGTCAGCGCGG  
CCAAATTCATCGAGCGAGATTCGTACACATGGCGCGCGGACATACGCTTCACCGTGGATCTGCTCCACAGGAGCG  
CCCTGTCCGGATCTGCTACGGGTAAAGAACTTACNTGGCNCTCGGTGCC

## .....:Rv153T7.seq:.....:

CTTTCGCGCCACCCACACCGTCAACGCCCGGAGTCGACGTCGTCAGGCCATCGCGGCTCACGGATGGATTGCG  
GCGCGGACGTGGTATCGACCGCGTCGGCGGACCGGAAACCTACACGAGCGCTTCTACGCCCGGATCTCGCGGAA  
CCGTTGTGCTGGTGTGCGGACCGCGGACATGCGGCTGGACATCGCGTGGTCGACTTCTCTCTACGGCGGTG  
CGCTGAATCGTGGTACGGCGATTGCTGCCCGAAAGCGACTTCCCGACGCTGATCGACCTTGACCTGCATGGCC  
GGCTGCCCTCGACCGGTTTCGTTTCGAACGATCGGGCTCGAAGACGTCGAGGAGCGGTTCCACAAGATGCATGGCG  
GCAAGTATTGCGTTGCTGGTGGTATGTTGATGGCGGCCATCGAGCGCGTCATACCCACGG

## Clone Rv154

.....:Rv154SP6.seq:.....:

ATACTCAAGCTTGATTTCGATCATGATGATCATCACCCGAAGTGTGGTAGCCGAGTGGTTATCGTGGGTACCGT  
CGTGCTTTCCATGGCGGCTCTTTCGGGCTTTCGATATTGCTTCGGCAGGACATTCGGGTATCGATGTTACTGGAT  
GGTGTGGCGATGTCGGTCTCTGCTGCTCGCGGTGGGATCCGACTACAATCTGCTGTGATTTCCCGGTTGAAAAA  
AGAAATTTGGGCGCGGATGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGGAGTGGTTACCGCTGCGCGCAT  
GGTGTTCGCGGTACCA

## .....:Rv154T7.seq:.....:

ATTGNCCTTCGGGCGCCATCGGTGAGGACGGCTGCGGGTGCTCAACGACGAGCTGCTCGCGGGACACACCTCGATGC  
TGCGCCCATGAGCGCGGTGGAACGCAAGCAGCTGATCGAGCTACACGCGCGCGGAAACGCTTCGCGCGCGGCGTGA  
CCGCGATCCGTTGACCGGGGCGGATCGCGGTGATCGTATGACGGCATCCGACCGAGGACGCGGCAAGCGCGGTG  
CGAGGTGCGCGCGGCGCGGTCGGGACAAGTGGTGGTGGCGGTCGCGCCGAGACGACATCGTGGCGGAT  
CGCGGCTACCGGATGAGGTGGTGGTGGTGGCGGACGCGCGGTTGCTTCGCGCGCGGCGAGGTTACCGCAACTT  
CACCAGACCTTCGACGAAGAAGTGGTGGCGTTTCTGATCGTGCTC

## Clone Rv155

.....:Rv155SP6.seq:.....:

ATACTCAAGCTTTCCCGTCCGTCATCGGCCAAGCGGTCGAGGCCAAGCGGCTGGTTACGACTCCCTGTTTGATG  
GACCATCTTACCAACTGCCATGTTGGGACGCGCGGACGAGCGGATGCTGAGGCTTACGAGCGGCTTGGTGGCTG  
GCCACGGCGCCGAGCGGCTGCACTGGCGGCTTGGTGACCGCAATACCTACCGGACGCCGACCTGTTGGCAAG  
ATCATCACCAGCTGACGCTGGTAGCGCGGTCGAGCGATCTCCGCGATTTGGAGCCGGTTGGTTGAGCTGGAACAC  
CGGACCTCGGCTCGAGTTGCGGACTTTCAGTGACCGGTTCAACCGGCTCAANAGGCGCTACAGATCCTCGAGCCA  
ATGGTCAAGGTGAGCGCCACGTTTTTCGGCGATTGGTACCCACGA

## .....:Rv155T7.seq:.....:

CGGCCACCGGGGCCATCGGCACAATCTGACCGGACCAAGATCTACACCATCGAATACGACGGCGTCGCGCACTTTC  
CGCGGTACCGGCTCAACTTTGTGTCAGCCTCAAGCGCATTCGCGGACCTACTACGTCAGCTCAACTACTTCACTCC  
TGACGCGGGAACAAATTGACGCGCGGTTCCGCTGACCAATACGGTGGTCCACGATGACCCAGTACTACATCATTC

GCACGGAGAACCTGCCGCTGTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGTTCAAC  
CAAACCTTGAAGGTGATTGTTAACTGGGCTACGGCGACCCGGCTATGGTTATTGACGCTCGCGCCCAATGTTGCGA  
CTCCGTTCCGGTGTTCGCCAGAGGTGAGCCGGTCTGTCATCGCCAGCGTCTCGTGCGCCGGGACCGACGAGGAATCGG  
CGATTTCGCCCTACA

## Clone Rv156

:::Rv156SP6.seq:::

ATACTCAAGCTTGGGGTGGCGCTGTGCGTGGTGTGCTTGGCGGCGTGGTATCAACACCGCCACGAAATGGGGCAC  
AAGAAGGATTGCTGGAGCGGTGGCTGTCCAAATCACCTCGCCAGACCTGCTACGGGCATTTCTACATCGAGCAC  
AACCCTGGCCATCANTCCGGGTGTCCACACGGAGGACCGGCGTGGCGCGGTTGGCGAAACGTTGTGGGAGTTC  
TGCGCCCGCAGTGTATCGCGGCTTGGCTCGGCCGTTTATTGGAGGCCAACGGCTGGCTCGGCTCGGCGTCAGC  
CCTGGAATCCCATGACGTATCTGCGCAACGACGTGCNCAACNGTGGCTGATGTCNGTGGTGTGTGGGGTGGG

:::Rv156T7.seq:::

TGCGCACGGCACCGCGGGAAGCTCAAGGCACCTACTGGCACCAGGCCACACAGTCAACCTGTGACCTCCTCGG  
CGGACCCCGCCGAGGTCTTGGCGTTACACCGAACGGCGGAGCGCGGAGTCTGGTACGCATCGAACAAAGAGCAAG  
GTGCATGGCGCGAGTTGTTCCGCCATTCGTGATGACGGGGTGCATCCATTCGAGGTTCGTCGCCGCGTGGTTCGAG  
TGGCGGTGACACTCCAGGTACTCGACCTCAGACGAGAGGACTCGATCCCATCTAGGTGTGGAGGAAACAGATCTTC  
TGTCCGACGACTACACACACCACCGAGGCTATCGCCGCGCCGCGCGATGCCAACTTCGACGCGGTACTGGCCCCGCGG  
CGCGCTCCCGGTTGTCAAACACTTGGCGTGTGCTTACGCACTGCCCAACATCGAGCCGA

## Clone Rv157

:::Rv157SP6.seq:::

ATGAATAGAAGAGCACATCCCTCAGTCGGTTATCATCACTAGCGCTCGCCGACCCGTGTAACCGATCATAGCGAG  
CGAACTGGCGAGGAAGCAAGATATCTGTTCTGTGATAGCTCTTACGCTCAGGCCAAGAGAATATCCCGCGG  
GGAAACACTCCAGGTAGAGGTACACACGGGATAGCCAATTGAGATTAATAACTGTGACACTCACACCTCATCAAT  
GATGACGACTACACCCGATATCCGGTACATGACGAGGGAAGAGAAGGATATCATCTGTGACAACTGCCCTCA  
AATTGGCTTCCTTAA

## Clone Rv159

:::Rv159SP6.seq:::

ATACTCAAGCTTGTGAACTCCTTCTTGAATACCGGCGCGCATCCACAGATGCCCGGAAGAACTTCCAGGTACCCAT  
GGCGCTGAGTACAGGGGCGGACAACTTGGTCTTGTCTGCTGAGTGGCGTGGTGTCCGGCTTGGACGGGCTCC  
GACGCTACCGAGGGGCGGCAAAACCTTATGCACTTGGGCGACCCGCGAGACGGTGCACACCTATCCGACCG  
CAAAAGCTCAGCGCGGCGCTCTTGTCTTCGTGCGATGACATTCACCACTTCTGACGCGGCTGGGCGAAGGAA  
GCAGAA

:::Rv159T7.seq:::

GGTATAGTCGTGACCGGTGACAGTTTCGACAATGTGGTGCCGTTGGCGGCTACGTGCCATCGAGACACTGGCGCA  
GGCTATCGCACCGTTATCGGCTACGAGCAATCGCGGTATGCTTCTTGAGCATGAGTCGGCGACCGTCTGTCATGGT  
CGACACCCAGCAGCGGAAGAGCGAGATCGCCGTCAAGCATGTGCGCGCGATTATCAGGACTGACCTCTGGCTGAC  
CGGCTATGTTGGTCCGATGCTGGCGCCGCGCGCGTGGTCTGGTGGCTCGGATAGCGAGGTGACGGAATCTC  
GTGGCAGCTCGAAAGGGTCTGCGCGTGCCGCTTTTGCGCAACGATGGCGCAGGTTACGGTCCGCGGGGTGGCGG  
CCTGGCGCGGCGCCA

## Clone Rv15

:::Rv15SP6D2.seq:::

GACACTATATNATACTCAAGCTTCAAGTCAATGTGCGCAAGCCCTGACGCTGGCCGACCGAGCCACCGCGCGGAN  
CCCTNTCTAGA

:::Rv15T7.seq:::

CTGTGACCACTGTTGCATCCCGCTCATGCCGACTCTGGTCATCTCGGATCCGCTGACACCCCGCTAAGGCTGCTC  
CTCTCGGTGCACTTACCTCAGCGCGGCAACNCCCGAGCTTTACGACTATCCGATGACGGCACTGTTGCGGCT  
AACTTCACCGTCAGCTTGGACGGCGCGCTACCGTGCATGGCGCGACGCGGGCGATGGCGGGGCGGCGACCGATC  
GTCNTCAACCTGTGCGGTGAATCTGCGACGTATCTGCTGGTGGGTCAGGCTGCGCATGAGGGCTATCCCGGG  
GTCGGGATGGGTGCTGCTCAAGCGCGCGACCGGACGGGCGGA

## Clone Rv160

.....:Rv160SP6.seq:.....  
ATACTCAAGCTTCGCACGCTCGCGCGCGCGGTACCGCCACAGATCGTCGATGTTGCGCTCGTCCGC  
TCTCGGCACCTGGTCTGTACCAAGTCAACGTTAACCGCGCGCACATGTCCTGCGCGCGGCAAAACGTGAAAAACG  
AGCGGGCGACTGCNATGTCATGACACCGACGGCCCGGATGGGCGCAGGCTTGGCAAAATCGATCTGTGCGGCCAGT  
GCCACAGCGTTCGCTCTCATACGGCGCGCGACGAGTTGAACCGACATGGGCGAGCGCTCGCCGTGCAAGTCCCA  
GCCACACGGGCGCGGCTGGCGGTGATGATCCAAAATTGAAAGTACGGAACCGCTGCACCAACCA

## .....:Rv160T7.seq:.....

ATCGTTTCGACACAGCGCTCCATCCGCGAGTGGATACTCCAGCAGGTAGCAGGTGCGCCACACGCTGGTCAGTGGC  
CGTTCAGCTCGCTTGGCGCGCTGCAGCAGCCAGTCCGGGAAATAGCTGCCCTGGCGCAGCTTGGGGATCGGCACGTG  
ATGGTTGCGGCACGGGTGTGCAAAATCAGGTGGCGGTAGCCGTTGCGCTGATTGGACCCGTATCGCTGCGTTTCGCG  
TAGCCCCCGCCGACAGGGCGCTCGGCTTCAAGCCCGCATCAAGCGCGCGATGAACGTGAGAGCAGCCCGCGAGCAGA  
TCCGGGCTCGCTGTGCGAGTTGGTCAGCCAGAAGCTGCTCGGTGTCGATAAGATGANAAGAGTATTCGCTTATT  
CCT

## Clone Rv161

.....:Rv161SP6.seq:.....  
ATACTCAAGCTTGGGTGTGCGCATCACCGAAGCGCATGATCAGCCACGTTTCGCGCGCGCCGGCATACGGCGGCG  
TACCGATCTCCGGCTCATACACCGCGGTAAATCGCCAGCGGTGCCGTTTCGAGCGCGAAGGTGACGACGCTGATTG  
AATCGAGTTCAGGTCAGCGGGTGGCGCAGCAACGGCGGAGCTCAACNACGTCAATCAGCTTGTGCGTTTTCACGG  
TCACGACCGCGGTGACCGTAGTGCCTCGGTGCGCTCGCGCGAGAAGTTGACCGCGCACCGCGCAGCAACGCTTTCGA  
CGCGACGCCACCCCCGGAT

## .....:Rv161T7.seq:.....

GCGCAACACGCTCGCGCGACGCCACGACGCTGCTCGGTGCGGTGCGCGCGCGAGATCAATTCAGGCAGCTCCCGGA  
CAATCGCGCTCTGCTGGCCCGCACAAAGGACTCGAGGTCAACCCCGGTGCCCGGGTTCGTGGTGCACTTCGCGATCGC  
ACAGGTTGGCCCAACACCGCGCTTGATGCCCGGTGCGCAAGCCCGGCAAGTTCGCAAAACCCAGCGTATCAGGCTCG  
GCTCGCGAGTTTCGCGGAAAAAGTGGCTCGCTGATCACCTACCATCGGCCAGGATCTGCGTGTGATCAGCAGCGTTCG  
CAAGGAGTTTGTGTGCTATCGACGGCTTTAGCCAGATGTTCCGGAATCGATATCCGATAGTGTCCGCGCCAAT  
GACTTGTATGCCCGCGGTGAGTGGCTGCCGCT

## Clone Rv162

.....:Rv162SP6.seq:.....  
ATACTCAAGCTTTCGCGATACCGGCATGTCGCGCACATCCAGACTTTCGGGGGATCCGCTGACAGCGCGGGAT  
CCCAAAGTCGGGATGATCGGCGCGCTACGTCGTGGTGTACCTCGTCGGTAAACAAACCGAAGCGTATGACTCG  
TCCAGCGGTGCGGCACATGTTGGACACCAACCGCCACCGCAGGGGTGAAGCGCTATGTCAAGCGTCGCGCAGCAG  
TCAATTGCGCACAGGCGGAGGCGGCAAAAAGTATCGCTAAAGTACCAGCGATCACGAACATGGTATTCGACGAA  
TGTGCTAGTGATCTATCGCTCG

## .....:Rv162T7.seq:.....

CATAGACACCGCGCAGCGGACGACGAGGCCAACTCCGCCAGCAGGCGGTTGGACTTGTGCTGTGGACAAGGG  
TTTAGCGCGCGAAGCAGTGACGTACATCGGCGAAGAGCAGTTTCGCTGTGCGACCGAGCGGCGAAACCGTAGGCTAGG  
GAAGCGAGGAGACATGGCGCGCGACCCGCAATGTACACGCTGCAAGCAAAACCATCGAACCCGGATGGCTATACATCA  
CGGCCATTCGCGCGGTCAAAGCGGATGTCGATGACGCGGAGTACTGATTACGTGCGCGGTGAATGCCGCACCC  
CGGGAGGACATTTCCGCCAAAATCAACCGGTTGG

## Clone Rv163

.....:Rv163SP6.seq:.....  
CGGGTGCATTTGGCCACCGCGCGCGCTGTCGGGAAATGGCGGGTCCCGGTTGTTGCTGAGGAGTGTGTAACCG  
TAGTTCGAAGTGGCGCGCTCAGACTCCACCGACGACGAGCGCAANCTGAATTCCTCAACCGGTTGTGNATC  
CGGACAGGTTGGGGTGCCTTTGGGGCAATNACAGGTGGCGCGCGTGCCTTCGGGTGCGCGCGCGGAGGTGCTGCTTTG  
GGATCCCGCGTGGGATTCGCGNTGTTGGCGCGCGGTGTTGGGGGGGCAACACGTGTGTCNCGGTGCGGGTGGC  
CCT

## .....:Rv163T7.seq:.....

CCAAGATCTACACCATCGAATACGACGCGCTCGCCGATTCGCGGTACCGGCTCAACTTTGTGTCGACCTCAACG  
CCATTGCGCGCACTACTACGTGCACTCCAACACTCTCATCTGACGCCGGAACAANTGACGACGCGGTTCCGCTGA

CCAATACGGTCGGTCCCACGATGACCCAGTACTACATCATTGCGACGGAGAACCTGCCGCTGCTAGAGCCACTGCGGAT  
CGGTGCCGATCGTGGGGANACCACCTGCGGAACCTGGGTTCAACAAACTTGAAGTGATTGTTAACTGGGCTACGG  
CGACCCGGCCTATGGTTATTGACACTCGCCGCCAAATGTTG

## Clone Rv164

:::Rv164SP6.seq:::~

AGCTTCCCAGATTCCGGCTTTGGATCAAGACCCAGTCGCCGGGCGCGATCCGGNGCTCGGTGACTACATCAAGCCAC  
AAATCGACGGCTTTCGGGGTCCGATACCGATGACGTGGCGGATGTCAGATGTTGAGTTCTCGCGGGGGCGGATGCTC  
ACCTGGCGATCACCTGCCTCTCGTTGACGATCGATCGTCTATGCCGCGCTCTCTCGGGGAACAGGCNCCAGTACATC  
GCCACAGACGGGATCCACCCGCATTTCGGCTACGGTTCGTCTGTTTCGGTGTTCGGGATAGTCGGTCTTGGTACAGTGC  
CGGTATGCGGACCGGCTCTAGCACTGACCAATGGCCAAATGCGGGC

:::Rv164T7.seq:::~

CGGGGGGCTCTTAATAGTGTAGGAAGAAGCTCTACATATTACAGGAGGATTACCATGGCTCGTGGCTCGGGATCG  
ACCTCGGGACACCAACTCCGTCGTCTCGGTTCTGGAAGGTGGCGACCCGGTCTGTCGTCGCCAACTCCGAGGGCTCCA  
GGACACCCGCTCAATTTGCGCTTCGCCCGAACGGTGAGTGCTGTTCTGCCAGCCCGCAAGAACCAGGACGTGA  
CCAAGCTCGATCGCACCTCGGCTCGGTCAGCGACACATGGGACGGACTGGTCCATAGAGATTGACGGCAAGAAAT  
ACACCGCGCGGAGATCAGCGCCCGCTCTGATGAAGCTGAAGCGGACCGCGAGGCTACTCTGTTGAGGACATTA  
CGAGCGGGTTATCAGACGCCCGCTACTTCAATGACGCCACGCTCAGGCCACCAAGGACCGGGCCAGATCGCCGG  
TCTCACGTGCTGCGG

## Clone Rv165

:::Rv165SP6.seq:::~

ATACTCAAGCTTCAATAACAGGCTGTGTTGGGCGCACCCGGCTCGCGAGTTCTGCACGACCCGCTCAAGTCCGGCC  
CGCACCCGCGGCATCTCCGGTCACGACAGGGCCGCGGCCCGCGCGCAGCGACGCGGTGTTGCGGCAAGTTCCGCGTCA  
ATGATGCTGACCTGATCGGCCACCCGGGCGTTCTCGGCGTCTTCGCGTTCACTAATCGGCTGGCTCAGCAGCGCTCTCG  
ACAGACACCAACCCGAGTGGGACCAAGCTGCTCCACCAAGGACCCGACGGATGCGCTCACCTCACCGCTCCAGCGGTC  
ACCACGACACGGTCTGTGCACACGCGCGGGGCTTACCACCCAGGCGGTACCCGCCAGGCGGATCGCCACACCCGCC  
ACCATCCCCGATGACGACAGCGCGGGAGTAAGA

:::Rv165T7.seq:::~

CTGGTGTGTCGACGAGGCTAGTACAACTTCTCTCCAATGCTCTTGGCCCGATCGCGGGACACGAGGATGACCCAGGAC  
ATCTCGCCGCGGAAAGTACTGAAAAAGCTCACACCGAGTTCGTGCGACCGGTGGTGCCCTACCTGTGCAACCGAGGAG  
TGTGCCGACAAACCATCGGTGTACGTCGTCACTGGTGGTTAGGTGACGAGATTGCGCTGTTTGGAACACGACGGCGCC  
AACTTTCGACAAACCGCTGCTGACAAAGATGTTGCGGCGCGGTGGGCGGAGATCNCGATCTGTGCGGTGCGGAAAT  
GCTGGAATCAAGTTGTAAGATAAT

## Clone Rv166

:::Rv166SP6.seq:::~

ATACTCAAGCTTTCGGGCGTCGTCCACCTGACCCAAAAGCGCAGGTGCGCGCGCAAAGCGCCGCTGGCCGCGCA  
ACTGGTCCGGCTCGCCCTGGCGGACAACTAGTAGCTGGACATCGGAAACCGCTGCACCACTTCTCGGACGCGCTCAA  
GCAAAAACGGCATTTCC

:::Rv166T7.seq:::~

TTTCACTCTCATTTTATGACATGACTGGAGATCTGCTAGATTGACGATCCTGTGAGCGTGGGTACCGGATTCAAG  
CGGTCGGTCACGCCGCGGTGGTACCGCTTTGCGGCACTGCTCGGCTCGATTCGGGATCGCGCGGGAAGTGGCT  
TTCGCGCAACAAGATCGCGGCTATGTCGGCGGCGATGACCCGCGATGACGACGCGGATCCAGGAAAAACCGTTCCAAC  
AGTGTGGGCGGCCATCCCCG

## Clone Rv167

:::Rv167SP6.seq:::~

ATACTCAAGCTTCCGACCAAGTTGAAACAGCACCGATTTCGGCGAGCACTTCGTCAACTTCCAGGTTGCCCGCAC  
AAGTATTTCGACAAATTTTCCTGCGGGCGCGCGCGCGCGCGCGGAGGTGGTCATCTTGGCGGGGGCTGGAC  
TCCGCGCACTACCGGCTTTCGGCCGACGGGACACCGTTTGAAGCTGACCGCCGCGGAGTCTTGATTCAAG  
CGCGAGGTGCTGCGACGACCGGTGCCAACCGCGCGCTGCGCCCGGA

:::Rv167T7.seq:::~

GTGTGCTGTAATTGAGAGCTGAGCCTGATGCACTCAACTTACTGAGCATGCTAACGCTGGTGGTGGGGCTTGTTC  
CGCGGTGTCGCGAGGACACGCTGCGGGGCTAGCTGGGAGAGGCCCGGTCAAGCCCGGAGAGCAGTGTCTAGTCCG



CCAGCTTGACCGACTTTCGATGAGAAACGGCTTCTCGCCGATTGAACATGCGGTGTCTGACGGTCGCTGAGCAACGGCTCTCGGAGTCTCGCGCGCTGATTTCTTATCAACCGCAGGAGAGGCCATCTGTTGTCGCGCGCTCGCGGTCGCCCATCTGTCGACGGATCTGCTCAGCCACTCTCGATGACGGTCTGCCATCAAGACGGGGCAACGGTGTCTCGGAGATATGTTGCGGTGGGACAGCGGAGCCGGGTGCTGTGTGATACCCACCGTTGCATGACCAAGTTGACGCGCTGATCGGCTGAGCAACGGCATCTCCGCTACAGGTCGCGAAGCTTGGTG

Clone Rv169

```

:::Rv169SP6.seq:::

```

ATATCATCAAGCTTTGGTGTACGCCGCCGACCGCATACAGTGTCAATTGGCCACCGCGCGCGGTGTCCGGGAATGG  
CGGGTCCCCGGTTTGTCTGAGGAGTGCTGAACCGTATGCGAAGTGGCGCGCGGTGTCAATCCACCCACGACGAGCA  
CAGCGCGCAAACTGAATCTCCACCGGGTGTGCTATCGGACAGGTGTGGGGTGCCTTTGGGGCAATGACAGTGGCGG  
CGTGTGCTGTCCGGTGCGCCCGCGGCAAGTGTGCTGTGGGATCGCCCGGTGGGCAATGTGCGTGTGTGGCGCGCGCGG  
TGTGGGGGGGCAACAGATGTCTCGGTCGCGGGTGCACCCCTGCACCC

.....Rv169T7.seq:.....

GGGGCCATCCGCACAATCTGTACCGGACCAAGATTACACCATCGAATACGACGGCGTCGCGAGCTTTCCGCGGTAC  
CCGCTCAACTTTGTGCTGCACCTTCACGCCATTGCGGCGCTACTAGCTGATCCAACTACTTCATCTCGACGCGC  
GACAAATTTGACGAGCGGCTTCGCTGACCAATACGGTCAGCTCCACGATACCCGCTACTACATCATTCGACGGAG  
AACCTGCGCTGCTAGAGCCACTGCGATCGTGGCGATCGTGGGAAACCCACTGGCGAACCTGGTTCAACCAAACTTG  
AAGGTGATTTTCAAGCTGGGCTACGGGCAACCGGCGCTATGTTATTTGCACTCGCGCCGAATGTGCGACTCGTTTC  
GGGTTGTTCGACAGSTGACCGCGTGCTGATCGCGACGCTCTCGTCGCGGAGACCGACGGAAT

Clone Rv16

```

:::Rv16SP6.seq:::

```

[illegible]

.....Rv16T7.seq.....

CGCGTATCGGTGGTGTGCTTGGCGGCGTCGGTATCAACACGCCACGAATGGGACACAAGAGGATTCGCTGGAG  
CGGTGGGTGTCCAGATACACCTTCGCGCGAGACCTGTCATCGGCACCTTCTACATCAGGACACACCGTGGCCATCACGTC  
CGGGTGTCCACACCGAGGAGACCGCGCTCGGCGCGCTTCCGGCAGACGTTTGGGAGTCTCTGCCCGCAGGTGTATC  
GGCGGCTTGGCGTCGGCCGTTTCATTGGAGGCCCAACGGCTGCGTCGGCTCGGCGTCAGCCCCGGAATCCCATGACG  
TATCTGCGCAACACAGTGCTCACACGGCTGGCTGATGTGGTGGTGTGTGGGTGGGCTGATCGCGGCTCTCGGCCCG  
GGCGTATCCCGTTCGTATCATCAGGACGATCTTCGGCTTCAG

Clone Rv170

```

:::Rv170SP6.seq:::

```

ATACCTCATGCTTCCGGAAGTTCGATGGGTGCGGCGGGGAGNCCAGCGAAGTCGTAGCGTGGCCGTGTTCTTGgctTCGGATCATCTCTCGTACATGACCGCCAGCGGTGTTGGAGTGATCGTGGCGGGCGGCTTCATATGACACAGGATCATTCG  
CAGGTCACGGCAATTCTCGAAGAAGAAATCTTCCCAATCACCGGCGCTCGAAGTCGGCAACAGCTACCGCGAAG  
AATCTGTCGATCGGCTGGGTGTTATTGGCTGTCTCGGTGCGCGGCTGCAAGGGTATCGACACCCAGTTCATTCTCC  
GGGCTGGC

```

:::Rv170T7.seq:::

```

GGCGTCACAGCGTGTGCGGCACGGCGTCTTCAGATTGGTAGGCCCTGCAGTTTGTGCATCAGGCCGATGCCGCGGCCCTC  
GTGGCCACGGCTGTACAGCAACACACGCGCGCCCTCAGCGGCCAGCATGCCACGCGCGGCTGTACAGTTCGAGGCCCGCA  
ATCGACAGCGCGGTGACCCAAACATCATCGCGGTCAAGCATCCAGATGACACCGGACAGCACTGTGCATCGACTCGCG  
TGTGGGCCCGCGGACTCTCGCGCGGGACACGCGGCAATGTTCCAGCTTCTCTGATAGTGTGGTGTAGCCATGCGCGG  
AATCTCCCATCAGAGTTCGGAATCCGCGCTCGCGG

## Clone Rv171

.....:Rv171SP6.seq.:.....  
ATACTCAAGCTTCGCGCTCGCTGCAGGAGTGGGAGCCGAGGGCTGGAATCCGAAAAACGAGCCGGTGATCGCACTG  
TCGCCGATCGGGGCCGACCTGGTTGGTGTACCGATGAATCCGCACCCAAAAATGTGGCTGCGGTGGCGCTTTCTTGAC  
TCCTTGGCGTCGACTCTTTGGCAGCCAGCAGCGGTTGGTCCAGGATCTGGATGGGCAAAAGTTGTGCGGCCCGGCCG  
GTGACGGCCGATGAGCTGACCCAGGTGCACAGCGCGCTGTTGGCTGACTTGAACCCGACATGGATTGCCCCGGGTGG  
CGTCACCTCAAGCATTTCAATGGTTAT

## .....:Rv171T7.seq.:.....

ATGCGTCACCCCGATGCGCCAGATCGGGGCTTCGAAATAAAGCACGAACAGCGGGGCAAAACGTCTATCTCGGAGC  
CGGAAGGGCAATCAGCCGACCGTCGAGCAACGACACCGCGATAACCACTTAGGCGTTGAACGGCCGGCCAAACATT  
ACCGCTCCGTTGATAAGGTTTCGGTCTCTTCCCGCTCATCCCAAGCACTTGCGGCAAAATTTGAACGCTTTCCTGT  
CCGGGACCGGCCCGGGCTTTGGGTCCTCCGA

## Clone Rv172

.....:Rv172SP6.seq.:.....  
ATACTCAAGCTTCAATCGCGCCGCCAATCCAAATATGCGTCTAGCGTCTCGATGAGCGTCGGTCCGGCATCGGCTA  
GGGGCGCATCAGCTCGGTATGCAGGGCCAGATCGCCCAAGGCGTCGCCCATCAAGGGCGCGTTCCGGGCAAAAATTC  
CCCTATCCAGCAGCGGCCGCGCGCGCTCCGCNCCAGCCGCGCAGCGCGTTTCATCCCGGAGATCGCCTCGTAGCGCTG  
GGTGCGCCCGGTCAGCATGGGCGCCCTGGGGCCGATGACCAACGGGGCGT

## .....:Rv172T7.seq.:.....

TTCCGCGGGTCTGTAGATTGCGGTGCGCCACCCACAGGCACCTATGAACCGCAGCCACGATCGATCTCGGTGG

## Clone Rv173

.....:Rv173SP6.seq.:.....  
GCGCACCATCGCCAGTAGGTGCCGTGGTCGGCGCGTGCAGGCCACCGAGCGGAAACGCGAGTCCGAACAGCAACAG  
CAGGACCGGCGCAACAGGGCGGTGACCATGCCCCGGCGCTGAACATCAACACAGGAAGGGCTCCGCCGAGCGTCC  
GCGCGACC

## .....:Rv173T7.seq.:.....

CATCGTCGAATCTCGGTCCGGTTGNTAGNACCGCAGCACCAACAGCACCCACCGACCCCGGCTTACGCGCAACCC  
TTTAGTTATTGGCGTGAACAGCAGCGTAGCCGGTTGCCCGATATATGTGAAAAAATCGTTCCGACGTACAAAAAA  
GTTCTGACGTCGCGTCAACTCGAACTGCTCGGAAGTCAATGATGATCCATCAGTCAATATAAAGTCG

## Clone Rv174

.....:Rv174SP6.seq.:.....  
ATACTCAAGCTTGTCTGCTGCTCAGCGTATGCATCCAAACAGCGCATCGCGATCAACGATCAGGCGCGCGGATTTCGG  
GCCGCGGAGTGGCAGTGGCCAGATGCCCAGATGCCCCGTTTTCGAGAAACTTCAACGCTGAGCGCTGCTTCCATCGAGAG  
ACCGGTTGGCCTCTACAACCGATGCGACAGTTGGACCGGCGATGTTCCGACGAGCGCTTCACATACGGCAAGTNTGCG  
CGG

## .....:Rv174T7.seq.:.....

TTGTCCAGCGCGGGAATCGGGCAGGGAGACGACACTTCTGTTGCTTCGATCTGCGCAACGGGTAGTTGGCCGCGAC  
CAGCTGTTTTCGGGTGAGCGCGTTGAAAGTGTGACTTGGCAGCTTGGGAGGCCACGATCCCAGGCTCAAGCT  
CACAGA

## Clone Rv175

.....:Rv175SP6.seq.:.....  
ATACTCATGCTTGGCGCCTGGGTGGCAGGCCACTGCCACCACAGGACCGCGGTGCGGACGCGGCTGACGCGCTG  
GTGGTCAGATCTGGCCGGTCTGCTGTTGTATGCCAACTTCCCGCCGCGCAACTGCTGGTGGGCGCGGTTGTTGCG  
CTCGATTGCTGGCTGGGTGCTGACCCNCCGCNCAACACCGGTGGGTGGGCTGGGCTACGGCTGCTATTTCGGC  
CTGGTGTCTCATGCTCTGCTGTTGTCCTGGATGCGCGAGCTGGTGGGCCCGGGCCCTGGTTGGCATGGGACGAGC  
TNGCGCTGTTCCCGGCACTTTCGGTCTGTTGCGCGTCTGGTACCTCTGTTGCCGGTTGGCC

## .....:Rv175T7.seq.:.....

CGCCAAATCAGATATGTTAACCGATATCCGAGCGCGATAGCTGGCGGGCTCGGGTGGTGGCCAGCGCGCTGCGAC  
GAAAGTGTGACCGTCTATGAAACAGACACCACCGCGGCGGTGCGCGCTGCTACCTGCTCGAGATCTCAGCATCCG

AGCCGGTGTGATCGCGCTTTCGGCGTGTAGTGGGTGCGCCGCCGACCCCGGCAAGAGCCGCGCCGACACAAACCCCGGA  
ACAGGAAGTCCCGGTACCGCGCCGAGNACTTGTGCGGAAACNCGAGTGCTCAAACGCATCCTGCTGAT

## Clone Rvl76

:::::::::::::Rvl76SP6.seq:::::::::::::  
ATACCTCAAGCTTGGGCACCTGACTTCGGTACCCCTTCCGCCTTTGGCCAGCAGCAGCCACAGCGCGTTGCGCGGACCGA  
ACGTGGACATCAATAGCCCGGAATCCGTGTGTGCAAGTTGGTAAACGGTGTGATCCCAAGCTTTGCCAGCCTTTTCGG  
TAGTCTTTGGGCCCCACCCCCACAGTGCTTCGACGGTACGGTACCCATGATGGCCATCCAGTTGGCATCGGTGAGCT  
GATAATGCCAGCTGGTTTCGCCAACCCGGTAGCGATCTTGCGCGCTGCTTGGTTGCACTGATACCTATCGAGCAAG  
ACAGCCCGGTTTGGGACAAAATGACTTTTCGGATCTCTTCGCGCACTTCGATGGGGTCTGCGGGA

## :::::::::::::Rvl76T7.seq:::::::::::::

AAAGTCTGTGCGGTTTCGCTAAACCCGCGCGACACTCAGACGGTCTGGTGGTGGCGCATGGCACCGCGGCGAGC  
AAAGCGCACTTCTCCGGGGGACGACAGCAAGCGACCGCTAGACAAGAGGGGTCTGCGCAGGCAGAAACGTTGGTACA  
CAGCTGCTGGCGTTTCGGGCCACCGATGTTTATGCCGCCGACCGGGTGGCTGCCACAGACGATGGAGCCACTCGCC  
CGGGAAGTGAACGTGACCATACACA

## Clone Rvl77

:::::::::::::Rvl77SP6.seq:::::::::::::  
ATACCTCAAGCTTGGGTTCCACGCGCGCGCAGCCACGCGCTCACCTTTCCAGGAGACCTCACCTGCCGATCCGAAATGG  
AATCGGCCGTGACGGAATTGGCGCACCGAACACCCCAAGAGGTGGTGGCTTCGTGCGGAACCGTACCCGAGTCCGCG  
CCACGCTGCGCACGCGGACGTTCTACACCGCACCAAGATCCGAAAGCTGCAAGCTCCAGCAGCCGATCCGACGTCA  
TCACCGTCCGCGCCGGCACGCTCTTGACCTATTGAGCTGGATCGGCCGTCGGGTGGAGTGGCGGTAGAAC  
TGGCTTAGAACCGCGCGGACACCGCNCCTGGGCGGGGCGAATTCTTGACCGCNCGCGCC

## :::::::::::::Rvl77T7.seq:::::::::::::

CGCGGTTGGCGTAGTTGGAGCGGTGCGCCTTCGAGGCGCAATGATGACGATGACCACGCGCATCAGATGGCCACCGAG  
AGGACACAACAAGAGCTGACGAATCCCTCCTTGGCGGCGGGGGCTTGGGTGCGCGGTGCGGATGGGCGCGAAT  
TTACGGCCCGCTCCCGCAGCGCGCGGCAAGCAGGGTCCCGAGCGATTTGGCGCGGAATTAAACGATACAGGCCA  
CCGCGATACCTGCCATGCTTCGGGCATATCGATGTGCGGCCAGAACAGGCGCAAC

## Clone Rvl78

:::::::::::::Rvl78SP6.seq:::::::::::::  
CCAAACAGAGCATCGGACATACGAGTCAACTACCCGGCCAAACGGTGATTCTTGCCCGCGCTGACGGCGCAACG  
ACGCCAGCGACACATTCAGCAGATGGCCAGCGCTGCGCGGCCACAGGGTTGGTGCTCGCGCGCTACTCCAGGGTTC  
CGCGCGGTGATCGACATCGTCAACCGCCGACCACTGCCCGGCTCGGTTTACAGCAGCGGTTGCCCGCCGACGCGGAG  
ATCACGCTCGCGCATGCGCCCTGTTTCGGGAATCCCTCGCGCGCGCTGCGCGGCTGATGAGCGCCCTGACCCCTCAAT  
TCGGGTCCAAGACCATCANCCTCTGCAACAACGGCGACCCGATTGTTTCNAGCGGCAACCGGTGGCGAGCGCACTAG  
GCTACGTGCGCGGATGACCAACAGCGCGCGGTTTCGTGCGGAGCAGGATTAACGCGGAGCGCCCATAGATTCC  
CG

## :::::::::::::Rvl78T7.seq:::::::::::::

TAANACCCGTGAATTTGGGATGGGCAAAAAGGCCAAGCACCGCGTGCCCAAGAACGCCGGGAGGGACAATTCGCGGC  
GGTAGGGCTTCGCGGGGAAGGCCCGAAGCTACGGCGTTTCAACACGTCGCGTTCNCCTCCGACCCGGAACATTTCGG  
GATGGCAGCAACCTGGTAGCNCCTGGCGGGGCGATGATTCGACGCGTCGCGCGGGGTATGCGCGCCCGCGCGGCT  
ACAGTCTGAACCGCGATGACCATCGATGTGTGGATGACGATCCGAGCGAACCGGTTCTACACGCGGATATGTTTCGCC  
TCGCTGCGCGCGGTGGACCGGTGGGTTCTATCCCGGAGACCGACNTCCGATCGAAGCGACCGCTCTCTCGATGGACGCG  
GGCGCGCTACCCCTGGGTTTGTCTACCGCTTGGCGTGCGCCCAA

## Clone Rvl79

:::::::::::::Rvl79SP6.seq:::::::::::::  
GTCCGCAAAAGACTCAGCGCGCGACTTGTCTCGCAGCTGCGCGTACCAGCCACCGATTTCGATGCGGTGGTTCGCGGAA  
GATGCTCTCCGAATTCGACCGCGCGACTCCAGTTTCGCGGAGCATCCGCGATGCCAGCTGCGGCTGCGCCCTGCGCGC  
CAGCGCAACCATCATCGCGAGTTCTGCCACTGGGCGAGCGCCCGCCGCGGAAGTCCAAACAATAGAACTGCACCGC  
GCCCGCATCTGGGTTAGCAGCAACCGCATGATCAGCGTCGCGAGCGGTTGACTTGGCTTGGCGTGCACCTAC  
GACCAGGACATTCGCTGCGGCGCCGGCAAGTCGATGCTCAGCGGCAACCCN

:::Rv179T7.seq:::

CGTGGCCAGAACGCCGGGAGGACANTCTCGGGCGGTAGGGCTTCTCGCGGGAAGGCCGACGTCACGGCGTTTCA  
ACACGTGCGGTCGCCCTCCGACCGCGAACATTCTGGGGATGSCAGCAACCTGGCAGCTACTGGCCGGGCGATGATCTG  
CAGCGTCCCGCGGGTAGTCGCCGCCGGGCGGTACAGTCTGAAACGCGATGACCATCGATGTGTGGATGCATCATC  
CGACGCAACGGTTCTACACGGCGATATGTTNCCTCGCTGCGCGGTGGACCGGTGGGTCTATCCC

Clone Rv17

:::Rv17SP6.seq:::

ATACTCAAGCTTTGCGGGCGGCGCGAAATGTGAACGCACCAACCCGCCGCTGCGGGTGGCGGGCCACTCGACCT  
CGAATTTGCGCGCGGTGACCATCCAGCCGACGGCAGTTGGGCACCCGCCGCCCGTGGCGGCATAACTGTTGGCGT  
CGCGGTCAATAAGCTCGAACAGCACCGAAACCGACTCCACCACCGCGCGGTGCGCCTCAAATCCAGCGCGATCTCCA  
CATACCGGGAACGTCGGTGTCCATCGGGTTTCGGCTTGCCCGCAGCTGCACACACCGGTGGCCTCGGCCACCT  
TCGGCGCTTGAGCGCAGCTACNCATCTGACGATCATACCCGCCGCCCGGCTCAGGCTTGGCTCCGTGACCGCACG  
CATCGCCCGGTTGCGCGCACCGCGACGCCGTACAGCCGCGCGCAC

:::Rv17T7.seq:::

AGCTTGC CGGAGTGGGAACAGAGCGCGGTTCTACCGCGGTGTGCGGCGCGCGATATCGGCCCTTTTACTAA  
CCGAACCCGATGTGGGCTCCGATTCGCGCGCGCATGGCATCGACGGCGACGCCGATCGATGACGGCGAGGCTTACGAGC  
TTAGGGGTGTGAAGTTGTGGACCAACCAAGGTTGGTAGGCGACTTGCTAGTGGTTATGGCGGGGTACCGCGCAGTG  
AAGGCGACGAGGGGAATCAGCGCTTTGCTGTCGAGGCTGATTCCGCCGGATCAGCTGGAGCGGCGCAACAAGT  
TCATGGGACTGCGTGGCATCNAACAGCGGTGACCCGGGTTCTATCGGCTCNGGTTGCCAAAGACAATTTGATCGGA

Clone Rv180

:::Rv180SP6.seq:::

CTCAAGCTTGGCGATGCGGGCTGGCAGAAACTGGCCGGCGGGGTTGGCTTGTTCATCAAGGGTGGGTGCCG

:::Rv180T7.seq:::

CCGAAGGCCCGTTCCCGGGCGTTACGAAGCGATGTCGGTTGGCCACTGCGGGTGAATCTTGGCGCGCGCGCGGT  
CGTGGAAACGCCAGGTACCCGGCGCGGTACC

Clone Rv181

:::Rv181SP6.seq:::

ATACTCAAGCTTTTTCTGCTCATGAAGGTTAGATGCCTGCTGCTTAAGTAATCTCTTTATCTGTAAAGGCTTTTT  
GAAGTGCATCAGCTGACCGGGCAAAATAGTTACCGGGGTGAGAAAAAGAGCAACAATGATTTAGGCAATTTGGCGG  
TGTTGATACAGCGGGTAATAATCTTACGTGAATATTTCCGCATCAGCCAGCGCAGAAATATTTCCAGCAAAATTCAT  
TCTGCAATCGGCTGCATTAACGCTGACCAAGTTCATAAGCACTTGTGGGCGATATCTGTACCCAATCTGGAATAGT  
CAGCCATCTGTCATCATCTCAGCTGACGCAACCAAGCAACGATAATCATTTTCGTAAGTGACGAGCAGCTTACGACGCG  
GACTCCCATCGGCAATTTCTATGACACAGATACTCTTGACCGAAGCCGGTGTCTGTGACCA

Clone Rv182

:::Rv182SP6.seq:::

CTCAAGCTTGGTCCGACATGGCCGGGCTGGAGCCCGGTATGGCAAGGTTCCGCTCAATGTGGTTGTATGACGAG  
GACTACGTTGCGCTCAATCAGCTCAAAAGTCAACCCCGTGGCGTGTGCGCGGATGAAGGTGCGGCGCCGACGATG  
TGGGCGAGGCAACAGCTGAAAACTTGTGCGCATGGTTCGAGCCCTCATTTGGGCGGTTCGGGATCGGTTGCAACCGC  
GCCGGAGTGCCGCTGCAACTCAACACCGCCTTACCAGTCTTTTCGTCAAAAATGGCGTCTGTGCCGGGTATAC

:::Rv182T7.seq:::

CCGAAGCGTGGGAATCTGACGAATACCGGAGCTGCTGGACATTTGGCCGCGAGCTGCTGGAAGAGGAGACCC  
TGCACCGACCCGAGCTGGAAAGCATCTTCTGCTGAGCTCAAAAGCGCGCGGCTCACCATGTTGACGAGACTTCGGTG  
GCCGGATCCCGTCGACAAACGCCCATCAAGACACCGGGGAGATCGCGATCGAAACGCGCGCAAACTTGGGCG

:::Rv183SP6.seq:::

CGACTCGACAAGCATTTCTGACAGTTGTTTTGGCTCGGCATGGTTAGCCAAGGTTCTGCGGTCCCACAGATCATCTT  
GGTCCGATAGCGCTCGTCCGGGTATGCTGCCGCCGGGATTCTCGTGTATTACTCCCCCGAAAAACGCCACCGGTC  
CAGCGCTGAGGCGCGCGGTGCCATCACAACCTGAACCCCAACAGGGGACATGCTTAGCGGTAGGGGCGCGGCCA  
AGGCGCGCAGCAATCGCATCACTGGCTGCGCGTCACTATTAAACCAACCCGAGTTCACCTCCAGACCCCGAATGGCG  
CCCGGTGATTGATCATCTTGGCGACCGCGGATAATCCGGGATTGCCAGCCCAATTCGACTACCGCATCGATCTCGG  
CTGACCGCAGCGGTCCGATTACCGGAGCGCCCGANTACATCTCTCCAATATCAATGGGCGCAA

## Clone Rv183

.....:Rv183T7.seq:.....:  
GCGGTNTAGCTTCCGCTCGTACCGGCGACCGCGAGAGCTCTGTTTCCAGTGTGTGCTGGGATTCTCACGCT  
GCTGCTGAGTGGTGGCAGACCGCTTCCGCTTCGGGTTACAACGAGCCGCGGGGCTAGCATCGTGCAGCGTGAAGTT  
GGTGTCTCCATGGACTTGGGATGTGCTGAAACCGGTTACCTACGACTCCAAGCTGGCGCGTCTCGTCCGAGGT  
CGTTGCTTGGGATAGCCGGGAGGCCCGGATCCGCAATGACGGATTCCATGCCAACGCTCCGAGTTGCATGCGGATCGA  
CTACGAATTTGATCACCAGAACCATCGGGCGTATTACTGCTGAGTACCTGGTGGGGTGGGATGCTATCCGCG  
GGTGACAGCCCCGGCAAGCCGCCATCCGTGCTGCTGT

## Clone Rv184

.....:Rv184SP6.seq:.....:  
CTCAAGCTTGGGCGTGACGGCCACC GGGGCCACTCCGCAAACTCTGTACCCGACCAAGATCTACACCATCGAATACGA  
CGGCGTCGCGCACTTTCCGCGGTACCCGCTCAACTTTGTGTCGACCTCAACGCCATTGCCGGCACCTACTACGTGCA  
CTCCAACCTACTTCTATCTGAGCGCGGAACAAATTGACGAGCGGTTCCGCTGACCAATACGGTCCGTCCCAGATGAC  
CCAGTACTACATCTTCGACAGGAGAACCTGCGGCTGCTAAAGCCACTGCGATCGGTGCCGATCGTGGGAAACCCACT  
GGCGAACCTGTGTTCAACAAACTTGAAGTGATTGTTAACTGGGCTACGGCGACCCGGCCCTATGTTTATCCC

.....:Rv184T7.seq:.....:  
CGGGTGCTATTGGCCACC GGGCGCGCTCTCCGGGAAATGGCGGGTCCCGGTGGTTTGTCTGAGGAGTGTGAACCG  
TAGTCTGAAGTGGGCGCGCTCGAGCTCCACCCAGCCAGCAGGCGAGCGCAAGCTCAATCCTCCAACGGGTTGTCGATC  
CGGACAGGTTGGGGTGGCTTTGGGCAATGACAGGTGGCGGCGGTGCGTTCCGGTCCGCGCGGAGAGTGTCTGCGTTG  
GGATCGCCCGCTGGGCATTGCGGCTGTTGGCGGCGGCGGTGGTGGGGGGGCAACANGTGTGCGCGGTGCGGGTGGC  
GCTGCA

## Clone Rv185

.....:Rv185SP6.seq:.....:  
NCTTGATATTGGCGTCAACGGTGTGCGCACCGCGCTCTGCAAGTTGGTAGGCGTGCAGTTTGTGCATCAGGCGGATGC  
CGCGGCCCTCTGTGGCCACGATGTACAGCACACGCCGCGCCCTCACGGGCGACCATCGCCAGCGCGCGCTCCAGCT  
GAGGCGCGAATCGCAGCGCGCTGACCAACACATCGCGGCTCAAGCACTCCGAATGCACCCGGACCAAGCAGCTCGT  
CACGCTCGCGGTTGGGCGCGGCGATCTGCGCCGCGGACACGCGCGACATGTTCCAGCTCCTCGTAGATGCTGGTGTAGC  
CGATGGCGGAACCTCCCATGACGAGTCCGAATCCGCGCTCGCGCACCCGCTCAATGTGCTTCTCGTGTTCGCGC  
GCCATTCGATCAAGTCAGCAATGGTGATCAGCGCCAGACCGTGCTCNTCGCGG

.....:Rv185T7.seq:.....:  
CATAGGGCGCGGTACCCGGTACCGGCCCGCGGCTACCACGTGCCGAATGGAAGCGCAGTAAGCCCTCAACGCG  
CCACCGCTTTGGCCCGCGCGCCCGCGTAGGCGCATCGGCGTGGCGGTGGGCGCGCGCATCGACCTCACCAGCGG  
CTTTCGAGCTTTGTTCGATCAACCGCGCGCATGTCGAGGATGCATTGCAAGCATATTGGAATTTGTTTATCGG  
GGGCGCGCATCCGATCGCCCCCTCCCATGTTGCGTGAGCAAGCAGCGGAGTCTGTGCGGATCGATGGCCACGGGTTT  
CAATGGCGGATGTTCCGCTGCCCGCGACTGGCTCTTGGGAGAGCGCATCTAGCACCCGATCGCGGACAGTGA  
CCGAACCGCGAGTAGATGTGGAAGCGT

## Clone Rv186

.....:Rv186SP6.seq:.....:  
CGTCCTTTTCCCAAGATAGAAAGGCAGGAGGTGCTTCTGTCATGAATATGAAGATCTGGTACCATCCGTGATACA  
TTGAGCTCTTCCCTGGGGGTGCTTACCTTCCACNAGCAAAACACGTAGCCCTTCAGAGCCNNATCTGAGCAANAT  
GAACAGAACTCAGGTTTGTAAACGCCACCTTTATGGGCGACGACCCCGATCACCAGTGGAAATACGCTTTCAGCAC  
TGTCGAATCGCGTACCAACACATCAGCATATGATTATTGTTCAATTGTATAACCAACAGTGTGCTCAACCCGCTC  
CTCGAATTTCCATATCCGGGTGCG

## Clone Rv187

.....:Rv187SP6.seq:.....:  
CTCAAGCTTCATGTCGTCAGGCTCGGGTACGCTTCCGTGCGAGTGTGCGAGTGATAAATGACGACCGGACCTCGTC  
GGCATCTTCCATAGCCCGCACACCTTCAGTTGCTCACCGAATCCAACCGGTAGAGGTGCGCGAGCGCTCGGCATT  
GGTCATCGGATATGCCGTCGCGGACGCTCAGAGCCCTCGGGTCCGGCCAGCACTCCGACGGCTTCGTGCGGGTGGT  
GGCAGCAGCATGGGCGACCATCGCAATCAC

:::Rv18T7.seq:::

NCGCCGACGACCACGCGCGGGTCCGGCGCCGGGCGCCGAGGCTGCTCCGCTCGGTGATGGCACGCCACC  
GCGACACACCCGGCTCGCTACGTCGAGCCATACCGGGCGAGCTACATCGGCTCGGCCGCCAGTGTTCGGGCGCT  
CTTTCGAGGTTCGAGGTGCATACCGATTTCGCGATCCGCGACGCCACCCTGGACGACAGAACCGTGCCCTACGANTGCT  
TGTCCGGCGGGGCCAAAGAACGCTTGGCATCTTGGCGGATTGGCGGCGCGGCTGGTCTCAAAGAAAGACGCC  
TTCCGCTGCTGAT

Clone Rv188

:::Rv188SP6.seq:::

CGCCACGTTGATGGGCAACACCCCGATCACCGGTGGAAATACGTCTTCAGCACGTGCAATCGCGTACCAACACAT  
CACGTCATCATTAATTCGTCCAATTGTATAACCAACACGTTGCTCAACCGCTCCTCGAATTCATATCCGGGTGCG  
GTAGTCGCCCTGCTTTCTCGGCATCTCTGATAGCCTGAGAGAAACCCCACTAAATCGGCTGCTTNCCTATTCTCC  
AGCGCCGGG

Clone Rv189

:::Rv18SP6.seq:::

ATACTCAAGCTTCAACCGATTGACGCAATGTGCGAACTGACGGCGCCCGCATGGCCAAATCCGGAAGACCATCATTG  
GCCAGTGGCGGGCGCTAACAGGTTCCAGCCCCCACCAGTGGCGCTCGAATCGGTGCAACCCATTCGCAAGCCG  
GCAGGAAACACCGCGGAAGCGCAAAGGGCTGCAAGTTTCGCGCCCAATAGTGTCTCGCAACACGCTGCGCTGCA  
AAACCGCGCGCGCATCAGCGACCCGACGCGAGGTCGAGAGAGCTGCTCAGCGCGCCACATGGGTTGCCAATCGGC  
ACGGCAGTGGCGCGCGCAACCGAACGCGTGGTGATGCCACGCTCCGAGGAGCGCAGCACCCGCCAATGCG  
GAAGCCACGAAACATCGGGCGCATCCACGCTCAACCTC

Clone Rv18

:::Rv18T7.seq:::

AGCTTTTGGCAGGGTCTCCTTCGAATTCGGCGTGACCGCTATGGGTTGACGACGGGCTGGCGCGCACACCCACT  
GGCCCGGGTGTTCGCCCCAACCCGGATCATGGTAGCGAAAGAGATTCCGCTGTTTCGATGCTGGGATTTCGCCA  
CGCGGAGGCCATCGACCGCAATTAATTCGCCACCGGGGTGCGAGAGGTGCCCGAGTCCCGCTCCGTCGACGTCTCCGACGA  
TCCATTCGGGCTTCGCCGCTCGGGTGGCGGTAGCCGTCGATGAATCGCTGCCCGCGCTACCAAGAGTGATTCTGTC  
CCGTTTTCGGAAGTGCTTTCCGCGATCGACTTTCCGTTGACCTACCGGCTGGGCGCTCGGCACACACCCGGTGAG  
GTCGTTTTTGTTCAGTTGGCGGAATCCGTCCTGCTGGTTACAGCCGAATCGTCA

Clone Rv190

:::Rv190SP6.seq:::

ATACTCAAGCTTTGTCAACCAACTGTTCCACACGCGCTCCATCCGGCGAGTGGATACTCCGACGAGGTAGCAGGT  
GCCACACCGCTGGTCAGTCGCGGTTACGCTCGCTTGGCGGCTGACAGCAGCCAGTCCGGGAATAGTCCGCTGGCG  
CAGCTTGGGATCGCAGCTCTTATGTTGGGACCGGGTGTGCAAAATCACGGTGGCGGTAGCCGTTGCGCTGATTGGA  
CCGCTCATCGCTCGCTTCGCGCTGCGGCGCCGCGACAGGGGCTCGGCTTCAGCCGCCATCAAGCGCGCGATGAACGT  
CGAGAGCAGCCCGCGACAGATCCGGGCTCGCCTGTGCGAGTTGGTCAGCGAGAACCTGCTCGGTGT

:::Rv190T7.seq:::

CGTTAAGCCCCGAGGGCGCCGACGCGGTACCGCCAGGTGCGCCACAGATCGTCGATGTTGCGCTGTCGCGC  
TCGCGCAGTGGTCTGTACCAAGTCAACGTTAACGCGCGCGCACATGTCCTGGCGCGGGCAAAAACGTGAAAAACGA  
CGGGGCACTGCAATGTCATGACACCGCGCGCCGCGATGGGCCAGGCTCTGCGAGATTTCGATCTGTGCGGCCATG  
CCAGCAGCGCTCGCTCGTCAATCAGCGCGCGCGCAGAGTTGAACGACATGGGCGAGCGCTCGCCGTCGAAGTCCACG  
GCACACGCGCGCGGCTGGCCGCTCAGATTCCAGACTTGAAGTACGGAACCCGCTGCACACACAGCAGCAGCTCG  
AAACTGCAACCCCGCGCTTGGTAGCGCCGATCGGGAGCGGGCGGTGCGGGCGCTGGCGTCACTAACTACGTGACAT  
CGTCGAAGATCGATGGATCGGCTGCTCACACCACTCGCGCGCGCAGGCGCCATCGCCGCT

Clone Rv191

:::Rv191SP6.seq:::

AGCTTTTGAAGCTGCGCGGGGCGAGCTTCGCGGCAATTCTACTAGCGAGAAGTCTGGCCGATACGGATCTGACCG  
AAGTCGCTGCGGTGCGGACCCACCTCATTTGGCGATGCGCGCGACGATGGCGGCTGGACCGATCTGTGCGCGTTGCGC  
ACGGCGACGCTGGGTGGGTGCTCAAGTCCGGTTCACGCTTGGGCTTTGCGAGCGGTCGCGACGCTGGTCCGCGGTTGCGC  
CGCGAAGCGCGGGTTCGGTGCCATCAGGAATGCTCACCGCGCGGCACTGCACGCGCATGGCGCGGATGTCA  
GCCATCGGACATCATGCTCGCGTTCATCTCTGACCACTTCGCGGAAACAGCTGATTCCGCGACGCGCCAGCGCA

.....Rv191T7.seq:.....

Clone Rv192

```

:::Rv192SP6.seq:::

```

.....Rv192T7.seq.....

CGGTGTGGGACACCGGGCTCTGCAAGTTGGTAGGCCTGCAATTTGTGCATCAGGCCGATGCGCGGGCCCTCTGTGCCACAG  
GCATGTACAGCACACCGCGGCCCTCAGCGGCGACCATCGCACCGGCGCTCCAGCTGAGGCGCGCAATCGGCATCGGACG  
GGCGTGACCCAAAACATCCGCGGCTCAAGCACTCCGAATGACCCGGACCGGACCGCTGTCACCGTGCGGCTTGGCCG  
CGCGGATCTCGCGCGGGACACGGGACGATGTTCCACGTTCTGTAGATGTGTGTGTAGCGGCATGCGGCGCAATCC  
CATGCAGAGTCGGAATTCGGCGCTCGGCGACCCGCTCATGTGCTTCTGTCGTGTGCGCGCCCAATTGCATCAAGTCAG  
CAATGGTGTATCAGCGCGGACCGCTGCTCATCGGCGAACACGCAATTCATCGGTTGTGCGGCATCGAGCCCTCATCTT  
TTTGGCTGACGATCTCGCAATCTGCCCTCGGGGTTGACGCGCGCAT

Clone Rv193

```

.....
:::Rv193SP6.seq:::

```

ATACTCAGCCTTTGGGTGATAGCCGATACACGGGAAGCGCATGATACAGCCAGCTTTTCGCCGCCGCCGGCATACGGCGGG  
CTACAGCTACTCTCCGCGTCATACACCCGCGGTAATCCGCCAGCGTGCCTGTCGCGAGCCGAAGGTGACGACGCTGAT  
TGAATTGAGTTCTCAGGTCCAGCGGGTGGCCGATCCGCGCGAGCTCAACGAGCGTAATCACGTTGTCGTTTCTAC  
GGTCAACCGACCCGGTACAGCTNCTCGCGCGTGCCTCGGCCGATAAGTTGCACCGCCACACCGCGACACCGCTTGG  
CACGCGGACCCCAACCCCGGATCGGTGTGGCC

```

:::Rv193T7.seq:::

```

AGCTTGTCTGGCATCCGCTCAGTAGGCGCCCGCGCGTGGCTTCAGCGCCGCGAGATGCTCCATAGGCGGGCCGGTCTG  
AGTCGGCGCGCGCTTACCGCCACCCGCGAGGAGCTGCGCGGCAGCATCTCCGCCCTTACGCATTGCGCGATCACAG  
AGGATAATATACGCTCATATTCTTGGAGTGCTGTCGACGCAATCGTGCGATGACGATTTGATGGCATCGGCTGTG  
CTTCGGCGTAGCCCTCAGCAGCATCTCCGCTATCGTGTGCGCGTCTCAGCAGACCCGACCGCGCGCGGACGCCGTCTG  
GTTTGGACGNTGTCGCGCGCATCTCGGTCAGCTTCGGCTCTCGGATTCAGCGGC

Clone Rv194

```

#####
:::Rv194SP6.seq:::

```

ATACTCAAGCTTGCTGCAGCTTCTATGACTGCTCCCGAAACCTGGGGGTGTGCCTGCTGTGTATGCACGGCATACGG  
ACATCTCTCTCCCTGACGACCCCGCTGGAACACGAGCCATGCTTCATTCATCAGGGGTCAACCCCGAAGGGCAGCG  
ACGCCAAGTTTGCGCAGCTGTAACTTAGTGTCTTAGTTCATTTCGTGCAGCAAAACACTGGTCGCGCTTAGGA  
ACTGAATTGAAACTCAACCGATTTGGTGCGCCGTAGGTGTCCTGGCTGCGGGTCGCTGGTGTTCGCGCTGTGGT  
TCAACAGCAATGATGACCGGGGAGGTGCAACACTGCCAGCGCTCGCGCAAGTTCGATTGCGGGGGGAAGAAGAC  
TCAACGCACTGGGTGTCAGCCGCGGCCACCG

.....Rv194T7.seq.....

AGCTTGCACGCGAGACGGACACATTGCGAACATTGATGACAAAAATAGAAATCATTGATGGTTTGAGTCAACCAGGCCGA  
TCAAGCCTTCGCCGAGCCAAATTCCAATCAAGAGGCCCAAGCCCGTACCAATCAGCCCGGCAACAGGAGGATTCGGCTCA  
TTATCAGCCAAATAACTGCTCTCGGGTTACACCCAAACAGCGCAATATGGCGAAACAGGTCGCCGTTGCACGATCA  
TAATGTCCAGGTATTGTAGATAAAAAAGATACCCACCAACAGGCATCAAACTGAGAGCGGTTAAATTGACCGTAA

AAAGCTCCGTCATCTGTTTACGGTGTCCCGTTGGGTATCCGACGTTTCCATACGCACACCGGCCGCGAGCTTTTGT  
GGATCGCTGTGCACTGGCCCTCATCTTTGATGATCAAATCGATGTGGCTCAGTCTTCCGGGA

## Clone Rv195

:::Rv195SP6.seq:::

ATACTCAAGCTTCGGCTCAGCGGGCGCTGCTGGTAAAGTCGCTGACCGGTGCAGGTTTCGACAATGTGGTGCCGGTTC  
GGCGGCTACGTCGCATCGAGACATGGCGCAGGCTATCGCACCCGTTATCGGCTACGAGCAAAATCGCGGTATGCGTTC  
TTGAGCATAGTTCGGCGACCGTCTGTCATGGTCGACACCCACGACGGAAGACGACAGATCGCCGTCAGCATGTGTGCC  
CGCGATTATCAGGACTGACCTCTGGCTGACCGGCATGTTGGTTCGCGATGCTGCGCCCGGCCGCGCTGGTTCGTGG  
TCCGCTCGGATACGAGGTACGCAATTNCNTGGCAGCTCAAAGGCTCTGCCGTTGCCGCTCTTTCGCGCAACNA  
AGGCNCAGGTTA

:::Rv195T7.seq:::

TGATCGCGCATCACTGCTTCATAAACTGGAAGCAGCGCAGCGCTTCTTTTCGGCCGCAACATGAGCCAGCCTCTCG  
TCGGCGGTTCGGGTGCAGGTCTCGGGCAGCTCGCGCGCGCAGCGCTGACCTGAAACAGCTTCATATCCCGCG  
ACGAACGACGCCAGTCCGCTACGTAAACCCCTCCGCGACTGTCCATGGACAACAGCGGTTCTCCACCGACCGGCCG  
GGTGTGGGGTGTTCGGCGACCGCGCAGCGGTGGTCCACACTGCGCAGCGGCCGCGCGAGCCGTTACCGACACAGCG  
CGCCGAGCAAGTCCCGCGATCGCATACTCCAACGGTTCGGGTAATCGAGGTTACGCTGGCGTACTCTCTGTCGCG  
TCGGGAGGCTTGTCTCAGCAGCTCGCANACGGCAG

## Clone Rv196

:::Rv196SP6.seq:::

CAAAGCGCAACTGCTCGCGGACGCCACGACGTGCTGCGTTCGGATTGCCGGCGCGAAATCAATTCAGGCGAGCTCC  
CGGACAATCGCGCTCTGCTGGCCCGCAACGAAGGACTTCGAGGTACCCCGGTGCCCGGGTCTGGTGCACCTGCCGA  
TCGCAAGGTTGGGCCACAACCGCGCTTGATGCCCGGTTCGGCAAGCCCGGCAAGTTGCCAAGCCAGCGCTGATCAG  
CTCGGCTCGGAGTTTCGGGAAGAGTGGCTCGGCTGATCACTACCATCGCCAGGATCTGCGTGTCTTACCACG  
CCCGCAAGGAGTTCGTTGGTGTCTATCGACCGN

:::Rv196T7.seq:::

CCGGAAGCCGATGATCAGCCAAGTTTCGCGCGCCCGGCATACGGCGCGCTACGATCTCCGCGTCATACACCCGG  
GGTAATCCCGACCGTSCCGGTTTCGCGAGCCGAAGGTGACGACGCTGATTGAATCGAGTTCAGGTCACGCGGGTGGC  
GCAGCAACGCGCGAGCTCAACGACGTCAATCACGTTGTGCTTTCTACGGTCACGACCCGCTGACCGTNGTCCGCC  
GGTGGCTTCGGCCGAAATTTGACCGGCCACACCGCGAAACCGTCTTGACNCCGGAAGCCACCCCGATCCGTTGT  
TGCGGAGGTTATTTGGG

## Clone Rv19

:::Rv19SP6.seq:::

CCGGAAGCCGCGACGCGCAGGTATAACGCCCTCCGATATGGGTTCGACAACAGCGGGTCGACTCTGGGCTTCTAGC  
GTTCCGCGNCTCGCGACAACAGCGCGGTTCGAAACCGACATCTGTTGATGTCCTAGCTATCAGCTTCGGTACGCAAC  
CAATCGAGTCTAGCGCGGTAGTTCAGCCCCGATCTCCANGCTCCGCGGACGCAAGGCGC

:::Rv19T7.seq:::

CTGGTTTATCTCCCGTTGAAGTTCATCACCCGATGTGGCGGAGCACTGCCAGTTCGATCTCAACTACCAATCCGG  
CCGTGGCGGTTGCGCGCCCCGGGGGGTGGCGCAACTCGACGAGCGGTTCGGAGAAATCGCCAGCACCCCGCTGAAC  
CGCGACCAACCCGCTGTGGAGATGTACTTCGTTGAGGGGCTTGCCAACCAACCGGATCGCGGTGGTTGCC

## Clone Rv1

:::Rv1SP6D2.seq:::

CCGAGCAGTTGGGAATCGCTCTGCANCAACCAATATTCTGCGCGACGCTCGCGCAGACGCTGGACCGATTAGGCGTA  
CGCTCCGCTGAGACACACGGGGCACTCGATGACCCGACGCTACGCTCGCAGGATATTGTTCGCGCGGACCCCTC  
TCTAG

:::Rv1T7.seq:::

TATATAATCTCAAGCTTCGCGACGCCAACGCTCGCGCATGTTGTTAGCCGACCCGGCTTTCATATGGCACCGGTG  
CCCCACAGTCGACCTGTGAGTCTCTGCACCGCACTTTTACATAGAATGTGGATTGCCGGATTGGGGATGTCGCG  
ATCGCTCAATCTGATGTCGCGTTGTCCGCGAGGGCCATGTGGATGGGGGGAAGGATCCGTGGCTCCGGGATCACC  
ATGGG



## Clone Rv201

.....:Rv201SP6.seq:.....  
ATACTCAAGCTTGCAGAGTTCCGATGGGTGCGCGCGGAGCCCAACGAAATCGTAGCTGGCCGTGTCTTGGCT  
TCGGATCTATCCTCGTACATGACCGGCACCGTGTGGACGTGACTGGCGGCGGTTATATGACACCGAGATCATTGC  
CACGGTACGGAAATTCGTCCGAAGGAAATCTTTCCCAATGCACCGGCCCTCGAAGCTGGCAACAGCTACCCGCAAGA  
AATCGTCAATCGCTGGGTGTTATTGGCTTGTCTCGGTGCGCGGCTGCGAGGGTTTACACCAACCGAGTTTCATTCTCG  
GGCGTGGCGGCGCATTCGAATCGCGGTCGCGCTG

## .....:Rv201T7.seq:.....

GCACCGGCGTCTGCAAGTTGGTAGGCCTGCAGTTTGTGCATAGGCGGATGCGCGGCGCTCTGGCCACGCATGTAC  
AGCACCAACGCGCGCCCTCACGCGGCGACCATGCCAGCGGCGGTCCAGCTTAGGGCCGCAATCGACGCGCGGTGAC  
CCAAACACATCGCCGGTCAAGCACTCCGAATGCACCGGACGACGCTTTCACCGTGGCGTTGGGCGCGCGATC  
TCGCGCGGACCAACGCGACATGTTCCACGTCCTCGTAGATGCTGTTGTAGCCGATGGCGGAAACTCCCCANGACAA  
GTCGGAATCCGCGGCTCGCGGAACCGCTCAATGTGCTCTGCTGCTTGGCGCGCATTC

## Clone Rv204

.....:Rv204SP6.seq:.....  
TGGTCCGTGTGCGCATACCAATACAAGCGCGCGGCGACCTGACGCGGCGGCGCAACCAATCGGTGGCCATGCCATC  
TTCTGCTACCGGTCACGAGCGACCTTCTCCTGGCCGACGTAGTGCGCCACCCGCGCGGTTGCTGCCATCGAT  
CCGGTCAAC

## Clone Rv205

.....:Rv205SP6.seq:.....  
GGCGTGTGGCCACCGGGGCCACTTCGCGACAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCGCG  
GACTTTCCGCGGTACCCGCTCAACTTTGTGTGACCCCTCAACGCGCATTCGCCGACCTATCGTGCACTCCAATAC  
TTCATCCTGACGCGCGGAACAAATTTGACGCGAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACTAC  
ATCATTCGCGAGAGAACTGCGCGTCACTGAGGCACTGGCGATCGGTGCCATCGTGGGGAACCCACTGGCGAACT  
GGTTCAACCAAACTTGAAGGTGATTGTTTACTGGGCTACGCGACCCGGGCTATGGTTATTGCACTCCCCGCCAA

## .....:Rv205T7.seq:.....

CGTCCGTGNCCTCAANCGCGTGNNGCCGAAGCGGCTGGTTACGACTCCCTGTTTGTGATGGACACTTCTACCAACT  
GCCCATGTTGGGGAGCGCCGACGACCGGATGCTGGAGGCTTACACGCGCTTGGTGGCGTGGCCACGGCGACCGANCG  
GCTGCAACTGGGCGCGTTGGTGACCGCAATACCTACCGCAGCCGACCTGCTGGCAAGATCATCACACCGCTCGA  
CGTGGTTAGCGCGGTCGAGCGATCCCTCGGCATTGGAGCGGTTGGTTTGAAGTGGAAACACCGCCAGCTCGGCTTCG  
AGTTGGCACTTTTCAAGTGGCGGTTCAACCGGCTCGAAGAGCGCTACAGATCCTCCAGCAATGGTCAAGGTTGAC  
GCCCAACGTTTTTTCGCGATTGGTACACACCGAATC

## Clone Rv207

.....:Rv207SP6.seq:.....  
CCCGTTCGCGTGAACCGAGCANNGCGAGCANCTGGCGAGGAAGCAAGAAGAACTGTTCTGTGAGTAGCTCTTACG  
CTCAGCGCAAGAAGAAATATCCACCGTGGGAAAAAATCCAGGTAGAGGTACACACGCGGATAGCCAAATCAGAGTAAT  
AAACTGTGATAATCAACCCCTCATCAATGATGACGAATATCCCCGGATATCAGGTACATGACGAAGGGAAAGAGAAG  
GAATCAACTGTGACAACTGCCCTCAAATTTGGCTTCCTTAAAAATTACAGTTCAAAAAGATGAGAAAAATCCATGC  
AGGCTGAAGGAAACAGCAAACTGTGCAAAATACCTCTCAGTAGGTGAGAACAAATGTGACGAACCCCTCAAATCT  
GTGACAGATAACCTCAGACTCTCTGTGCTGATGGAAGTGATATCGCGGAAGGAAATAAGATNTGAGTCGCTGCGC  
GGCTTCTTTTCTCAATGTATGAGAGCG

## Clone Rv209

.....:Rv209SP6.seq:.....  
TGACACCCAAAGAGGGCACTTAAGATGGCAATGCGGCGCCTACCTGCACGTTTTCGCGATGTGAGAGGATGCCGAG  
GGAGAACAATGCGAGCACGGCGCTGACNITGCTCACCAGTTTGGCGGCGGTGACATTGGTGGTGTGCGGGCTGCN  
AGGCCGANTCNAGSCGGAAGAACACACGCGGCCGACCGCAATTTCTGCTCAGCCGCAAGCGCAGCTCAGCCGACG  
CGGTGGAGTACTGCTGCGCGCATCACGCG

## .....:Rv209T7.seq:.....

ACGGCGCAGCGCTGAGGTGGGCGCGCGGCTATTATGCTGTCTCCAGCTCAGCGACGCACTGGCGCAGACGGCGCCG  
CAACTAGCCACTCGGTGGGAAGAACACACGAGACTGCTGGCGGCTCGGATCTGGCTTACACGCTGGCGGCTGGCGCG  
GCGCACCGCGCGGTGCGCACCGCGGTGTTGCGCGCAACTGCGCGAGCTGCTCGAGGGTTTGGCGAGGTTGGCCGAC

GGTGACCCCTCTATGACGCGCGGTGGGACACTGTGATCTAAGACCGGTCTGGGTCTTCTCGGGCAAGGGTCTCAGT  
GGGCGCGGATGGGACCCCAATTGCTCGCCAGCGAACCAAGTGTTCGCGGCCACCATCG

## Clone Rv20

:::Rv20SP6.seq:::

ATACTCAAGCTTCGCGAGATCCGGATGGCACTCAGCTGGACAAGACCTTCACAAATCTGAAATCCTGACCCGATAC  
TTGAACCTGTGCTCGCTTCGGCAATAAATCGTTGCGCGTGCAGGACGCGGCGCAACCGTACTTCGGCATCAACGCGTCC  
GACCTGAATTGGCAGCAAGCGGCGTGTGCGCGGCATGGTGCAATCGACCAGCAGCTCAACCCGTACACCAACCCC  
GACGGCGCGCTGCGCCGGCGGAACGTGCTCCTCGACACCATGATCNAAAATCTCCCGGGGAGGCGGAGGGCTTGGCTG  
CGCCTTCAGGCGCAACCGTGGGGTTCTGCGCGACGCCAATGATTGCGCGCGGGTGCATCGCGGGCGCGACCGCCA  
TTCTTCGGAATACGTCCAGGAGTACTGTCTCGGGG

:::Rv20T7.seq:::

AGCTTATGTGGCGCCACCTACCTTATCTAGCCTAGCTAACTAAATCAAGTCCGACAGTGCAGCGGTGGCCACCCA  
GCATGAGGTTATGACCACGGCATATGCCAGCGCGTGGCGGCGATGCCGAGCTGACCGAGTTGGCGGCTAATCACAC  
CAGCCATGCGGTGTTGCTGGAGCAATTTCTTTGGAATCAATACGATCCCGATCGCGTCAATGAGGCCGACTATGC  
CGGGATGTGGATTCAAGCGGCCACACGATGATATCTATGAGGGCACTTCGATGCGCGCGTGGCGCTCNGCAGCCGA  
AACACCAACCGGCTCGGATGTTCAACGGCGGTGCTGGCGTCTTGCACGCGCTGCCGCGATCTC

## Clone Rv214

:::Rv214SP6.seq:::

ATACTCAAGCTTGCCACCCATGCCGAGCAAGTGCAGCTCAGCGATGACGAATGTTCTTCTCGCGGTGTTGCTGCTG  
GTTGCGGGCTATGAGAGCACTGCTCATATGATTAGCACNTTGTCTGACGCTGGCGGACTATCCAGATCAGCTGACA  
TCTCTTGCGCAGCAACCAAGCACTGATCCGTCGCGCATCAGGAGCACTTCGCGTCTTATATCGCAATCCAAACATCT  
GCGCGACAAACGCGGTGCATATTTCGCTCGGTCAAGCGGTCTCCCGGA

:::Rv214T7.seq:::

CGGGGTAGAACGATGCGATCTGGGCCATGTCGACATCGGTGGTACAGGTAAACCGCGCGGTGTCGCGGCTCTCGGAG  
ATCAGAACGTGGTTCGAGTTGACACCGCGGGCTTCAGCCAGTCGCGATCAATCGCGAAGTTCGGCGCTCGCCGCCCA  
ACTAGCGCGACCTCGCCACCTAGCACACCGATGGCGAAGGCCATGTTTTCGCGCCAGCGCGCGCGGTGCATCATCAAC  
TC

## Clone Rv215

:::Rv215SP6.seq:::

ATACTCAAGCTTGGCGGCAACGCCACTACCGGGTCTCAGAGTCTGTGCGGCCACCGCGCGCGCGCAAGACCATC  
AGGTCGTAGTTGTCTGGACGTTTCGACACCGTAAGCGAACAATGCGCGCGCCATGCTGTGCCGAGCAGCATGCGC  
TTGCACCCGGGATATTCCCGGTTGGCGATCCCAACGAGGGTGTGCAAGTCAGCGGTGTATCTGAGATGTCTCTCACTA  
TCATCCGTTTGGCACCGAGCGGCATGCCCGCGGGGGTCAAC

:::Rv215T7.seq:::

TCGACGCGCATCAAGTTCGCGAGTATGAGTGTTCATCTACCCAGGAAGGCGTGAAGTGGCTGATACCGTGGCTTGA  
GATTGCGTGGGGTGCAGTAAATCCGCCGTGTGCTCGGATGAGCGCGACGTTAACCTTGAATGTGCTGTGTCG  
TGGCTGTGCTTGTGATGAGCTGTCTAAGTGGTGGCTAACCGTTTACGAGCGCGCGGCTCGCTGCAAAACATGAA  
GCCCGCAGTCTGGGTTTGTATTACACAACGAGGGCGTCCCGATCTGGCGCGCGAACGAGGTGCNCACTATCCA  
TTGAGGTGAAGTGCAGTCTTGTGCTCATGCCGTTGCGGTTTGTGTC

## Clone Rv217

:::Rv217SP6.seq:::

ATACTCAAGCTTCGCTTCGATGAAGTATGTCGTGCGTCAGCGCCGCTCTTCGAGCTCCTTGGCGATGCCAGCAAGGA  
GTGATCGCGCGGAGCTTGGCCAGGATCTTGTGCGCTGTTCCTTGACGATCGGGGCCGCGGATCGTAGTTCTTGTA  
GACACGATGACCGAAACCCATCAATTGACCCCGGCGTCGCGGTCTTGACCTTGGCTTACAAACTCGCTGACGTGCT  
GCGCGTGTGCGGAATGCCTC

:::Rv217T7.seq:::

NTCAAGCGCAGCATGCGCGAGGAAACGACGAACCAACAGCCATGGTGGTGGCGCGCTCGAGAGGTGGCGGTCG  
CCACAACGGGAAGATCGCTTGAGCGTCTGACCGCGGCTCGAGTTGGGTCTAACAAGTAGCTGATGCCGATC  
ATGTCAGCTTTCGTGCTCAGCTCAGCGTGCAGCGCGACCACTCGACGAGGTCTCGGTGCGCGCGCGCGGACGCGC  
AGCAGTGACGATTCAGGCGCGTCCGG

## Clone Rv218

:::Rv218SP6.seq:::~

CGATAATCGCTTCGGGTAAAGTCAGCAGCTTTACGACGGCGACTCCCATCGGCAATTTCTATGACACCAGATACTCTT  
CGACCGAACGCCGGGTGTCTGTGACCACTCAGTAGAAAAAGAGGATGAGATCTCCCGGTGCGCTCTCAGTAAGCAGC  
TCCTGGTGGGTTCATTACCTGACCATACCCGAGAGGTCTTCAACACTATCACCCCGGAGCACTTCTAGASTAAC  
TTGCCATCCGACCCATATAGGCTAAGGTAAATGGGCATTACCSCGAGCCATTACTCTACGGCGCAATTAACGAAT  
CCACCATCGGGGCGGTGCTGTCN

## Clone Rv219

:::Rv219SP6.seq:::~

NAATACTCAAGCTTTCTCGTGATTACCAACCGGTGTAATTTGGGATGGGCAAAAAGGCGAATACCCGCGTGGCCACAAA  
CGCCGGGAGGGACAATCTCGGCGGGTAGGGCTTCTCGCGGGAAGGCCGAAACGTACGGCTTTCAACACGTGCGGCTC  
GCCCTCCGACCGCAACATTCGGGGATGGCAGCAACTGGTATCACCTTGGCGGGCAATGATCTGCAGCGTCGCGGC  
GGGTAGTGNCGCCGGGCGGTAC

:::Rv219T7.seq:::~

CCAACCTAGAGCATCGGGACATCGAGCTCAACTACCCGGCCAAACGGTGATTTCTTGGCGCGCGTGCAGCGCGGAACG  
ACGCCAGCGACACATTCAGCAGATGGCCAGCGCGTGC CGGGCCACGATGTTGCTGCTCGCGCGCTACTCCCAGGGTG  
CGCCGCTGATGCACATCTGTCACCGCGCACCACTGCGCGGCTCGGGTTCACGAGCGGTTGCCCGCCGACGCGGACG  
ATCACATCGCGCGATCGCCCTGTTGCGGAATCCTCGGGGCGCGCTGCGCGGCTGATGATCGCCCTGACCCCTCAA  
TTCCGGTCCAAGA

## Clone Rv21

:::Rv21SP6.seq:::~

ATATCTCAAGCTTGTCTGAGCTTCTGTGACTGCTCCGAAACCTGGGGGTGTGCCTGCTGTGTATGCACGGCATACGG  
ACATCTCTCCCTCGAGACCCGCGTGCAGACGACCACTGTCATCATCAGGGGTCAACCCCGGCCAAGGGCGACGGC  
ACGCCAAGTTGCCCGACCGTTAAGCTAGTGCTGTTAGCTTCATTTGCTGCGAGCAAAACAGCTGGTGC CGCGGTTAGGA  
ACTGAATGAACATCAACGATTTGGTGCCGCCGTAAAGTGTCTGGCTGCCGCTGCGCTGCTGT

:::Rv21T7.seq:::~

AGCTTGGCGCGGTGGCGATCGGGTTCAAGGCGCGCTCTTCGAGCAACAACGAGCGAAGACGCTCGCGGACGGAGCC  
TTTATCGACATCCGTTGCGGCTGGCTGACCGCGCGGAAGAACTGCTGGACGCGTTGTTGTGACAGGTGCCGTGGCGA  
CGCGAGCGCGCTCAGATTCAGACACCGGTTGTCATGTGCCGGGCTGTTGAGTTTTCAGCACTGACATCGAAGAT  
CCGCCCATCCGACGTGCGCGGATGCGCC

## Clone Rv220

:::Rv220SP6.seq:::~

AATATCAAGCTTGGCGAGCAGGAGCTCGAGTGGCGCTTGCAGTGACTTGGCGACCTCAAAGGCCACCGGTACCC  
CGCCGGCGGCAAGCCAGGACNACNAGGCCCTTCCGCGATAGCTGCGCAGGCGTGGCGCAACTGGCGTCCAGCGT  
CGCCACGATCGTCAAAGAGCTTCATCTGCGGAGTGTGTCGCATCTCATGGCTCAAATATGAATTAAGTCCCTGGG  
CGACTGACGACAGTCCCTCAGCAGCAGGATTGCGCATCCGCGCTTTGACGCTGCTCCGCAAAATCCGGGCTTGCCTG  
CGCGAAGCGAATCGCGCGCGCTACGCTGGTGGCTCACTTGGCGGCTG

:::Rv220T7.seq:::~

GGTGTGGCGGTCCACCTTCGCGCGCGCGCGCGATATGCTTGTGCTGTTGCTCATTGATATCAATCTATGGGT  
CGTGGTTACTCAGCGGGCGAAGCTGGCCCTCCCAGGGTAGGGCCCTATTGCAGCGGTGATGCCCATCGACCGAGCGG  
TACCGCGCATGATCTTGGCGAGCGCTGCAGCTGCTTGGCGTTGAGGTCCGCTCTTGTGTTCCGCGAATTTCCGCGA  
CTTGATCCGAGTGACTTTGGCGACCTTGGTCTTGTGCGGCTCCGCGAACCCTTGCACACACGAGCGGCTTAAGCA  
GCAGCTTGGCGGCGCGCGGCTCTTCAGCGTGAAGTGAAGCTACGCTCTTCATAAACGCTGATCTCCACCGGGATGA  
CGTTGGCGCGCTGTTCTCCGTGCGCGGCTTACGCTTGCAGAACTCCATGATGTTGACCCGTGCTGACCGAACGC  
GGGCGCACTGGCGGGC

## Clone Rv221

:::Rv221SP6.seq:::~

ATATCTCAAGCTTTTCAGCCGCAAGCGCGGCTGCGCCCTCTCGTTCGCGTGCCCGGTGCTGCTCGATCGGTTCCGGGT  
CGCGCGCTAGGCCCAATTGCCCGGCTCTCTCGGGCGGTTCCACAAACCGCATGCTGCGCGGCTAGGTTCAAGCG  
ATGCCGTAAACCCAGGACCGATGCTGATCGGCTATGCAGAGGTCAACCAAGGCGCATGCGACGCCNAAAT

CAGTCCATCGAACCCTCGACCTGATGGCCNCCGCGGCCGGAAGCCGCCGAGTCCACCGTGCTCGAAGCGGTGGAT  
TCCATCCGTGGTGGTGCACATGCTGTGCGCGCAATTACGGAAATCCCGGGCGTCTCCTCGGG

.....Rv221T7.seq.:.....

NCCTGGTTTCATGAACCTGGAAGCAGCGCAGCGCTTCCCTTTTCGGCCGCAACATGAGCCAGCCTCTCGTCGGCGGTGCGG  
TGCAGCTCTCGGCGAGTCTCGGCGCGGACAGCCGCTGACCCGAAACAGTTCATATCCCGCGAGCAACGACGCC  
AGTCCGCTACGTAAACCCCTCCGCGACTGTCCATGGACAACAGCGCGTTCACCACGACCGGGGGCGGGTGTGGGGTG  
TTCGGCAACGGCAACCAAGTTGGTTCACACTGCCGACGGGCGCGCAARTCCGTTCACCGAACGAGCGCCCNAAACA  
ATTCCGCCGATCCCATAT

Clone Rv222

.....Rv222SP6.seq.:.....

ATACTCAAGCTTTCGGGATCAATCTCGAGGGCATCCAGCGACGAAAGTAAACTCTATCAAGCTTTTTCGACGACCC  
CAGCGACGCCCATATATATGTTCCGGTGGGCAAGACGGTCCCTACCTGGAAAGTTCGTTGGCGCGGACACCGGTGAG  
CCCACCGCGCAGCGGGGCAACCTCAGCGACTCGATTACCCCGGACGAAGTACTCTACAGGTGGCCGAAGAGCTCTTT  
GCCACACCGCAACGAGGACGACTTTGGGCTTGGACCCAGAAACCGGCCACGAAATCTTTGCCAGGGGAAGGCCGGTT  
TGGGCTTATGTTACCTATATCTGCCGGAACCTGCGGCTGATGCGGCGCGGCCGCTCAGGGAN

.....Rv222T7.seq.:.....

AGCAGCTAGCCGCGCTCGCCGCGCTGGTGGTGGTGTGCTGCGAGCCGGATGCACCAACGTGGTGCAGCGGACCG  
CCGTGGCTGCCGCAAAATCCGACCACTGCATCAGGATCCGATACCGGTTTCAGCGCTTGAAGGGCTGCTTCTCGACT  
TGAGCCAGTCAATGCGCGCTGGTGGCGACATCGATGAAGTGTGGTTCAACGCAAGGCAATGTGGGATGGAGCA  
AGAGCGTGGCCGACAGAATGCTCGGCTATCGACGCTCCAGCACAGGAAAGGTCTATGCCGCGCACGGGTGGACC  
GCTATGCGCGGCCAAGCGCTGATGACAGCATCGATGACTCCAAGAAACGCGACCATACGCCATTCAAGCGGTGCTG  
GGCTTCCGACCGCACATGATGCCGAAGAATCTACAGCTCTCCG

Clone Rv223

.....Rv223IS1081N1400.seq.:.....

CGCGACTGGCTCCCGGNCGGCTGCTCGGGTCCGCGATAGAGACCGGGATCTCGCCGACGACGGGCGAGCCGGGTTG  
CGTGGGACGGGCGGGGGTTCGGGCGAGCCCAAGCAACGGGCTAGTCCCGCAATCCTACGGAGCGCTCACCTACGCCCTAC  
GTAATAGTAGCTATCAATAACAGTTGACATACGCAACGATCTGTGAGATCAATATTGCTGAGCGATGTCAAGACAGG  
CGTCAAGACAGGTGTCAATAATTGCTCGCTCGGTGGTACGGTAACCGGTCTGCGGGTGTGTGACGCCATAAGGAAGGAG  
TGTGGTGGTGACGCTGAGAGTGGTTCGTAGGGTTTTCGCGGCCGCCAGTGGCGGGTGGAGGCGTTGACCGACCGGC  
TGCGCGCGCACAGCTGGCGCGGCCGCGGATACGCGCGTGGTGGCGCCCGCGCGGATCCGGTGTCTGTTGCAGA  
ATGCGTGGGGTTTACGCGCTTAAGTAGCCAGCATGCCGCGATCGCCGGCGAAAGGTTCAAGAAGTGGT

.....Rv223SP6.seq.:.....

ATACTCAAGCTTATTGAACCGCGGTCGAGGCAAGTGGACCTCATAACGACTCGGGTCCAGCGACCGGCCAACAC  
GAACGGCGCGGACGACTGGGCGAGGTCGCGGCCCTCCCTTCAAAACAGGATCCGTTGCCTGGCAACGACAGGCTCCGG  
TGGCGGTTTGGGCGCGTCTGCTGCTCCAGCGTCCGGTCCGCGGTCGCGCGGACGCTGTTTCTCCATCTCGCCCC  
CTAATCTCGAGCGAGCGCTACCCGCGAGGCAACTCCCAAAATGCAATCCGCAAAATGCAATCGGTCNAGCTATTT  
CTCACACGACCGCTAGTTGCGGATCAGAAATCCGTTGGGCGCGGAAGTCCAGCCGAATTTGTTCTCCGCTCCGCAT  
CATGCTTGAATCGTTTGGAAATCATCTCTATATGCTCGATCGCTTCATAGGTTCCAGGCCCCAACCCGGGAGGA  
CTGGGTGGCCGTTGATGTTGGAATCTCCACTACTAGTATTACCGGC

.....Rv223T7.seq.:.....

GTCCTCGATCATGGCAAGAGCTGACGAAGCCGTAGAGCGCTTTCGGACCCGCCGCTCGATGCCGCGCCGTATACC  
TTCTCTCGCCCGGACGCCCTGGTGCTCAAGGTGCGCGAGCGAGCCGCTGCGGGGTGCACACCTTGATCGCCACC  
GGCGTCAACGCCGAGGGCTACCGAGAGATCTGGGSCATCCAGGTCACTCCGCGAGGACGGGCGCTGGCTGGGCG  
TTCTTCCGCGACTGTTGTCGCCGCGGGCTGTCGCGGTCGCGCTGCTCACCGGGACGCCACGCGCGGCTGTTGGCC  
CGGATCGGCGCCACCTTGCCGCGCGGCGCTGGCAGCGCTGCAGAACCCATACGCGCAATCTGATGGCAGGACCC  
CCGAAGCCCTCTGGCGGTGGGTCGCGACCTGCTGCACTCCATCTACGACGAGCCGACGCGCAATCAGTTGTTGCC  
AATATGATCGGGTTCTCGAC

Clone Rv224

.....Rv224SP6.seq.:.....

ATACTCAAGCTTTCGTGAGTTATGGCGCCAGCAGACCAAGAGCATCGGACATACGGAGTCAACTACCCGGCCA  
ACCGTGATTTCTGGCGCGCGCTGACGGCGGACGACGCCAGCCACCATTCAGCAAAATGGCCAGCGGCTGCCGGG

CCACAGAGTTGGTGCTCGGCGGCTACTCCCAGGGTGGCGCGTGATCAAGATCTTACC CGCGCACCAGCTGCCGCGC  
TCGGGTTACAGCATCCGTTTGGCGCGCGC

:::::::::::::Rv224T7.seq:::::::::::::

GCCCCGTGTAATTGGGATGGGCAAAAGCGAAGCACCGCTGGCCACGAACGCCGGGAGGGACAATCTCGGCGGGCT  
AGGGCTTCTCGCGGGAAGGCCCAACGTACGGCGTTTCAACACGTGCGCTCGCCCTCCAGCCGGAACATCTCGGGGAT  
GCCAGCAACCTGGTAGCACCTTGGCGGGCGATGATCTGCAGCGCTCGCGCGGGTAGTCTCCGCGCGGGCGC

Clone Rv225

:::::::::::::Rv225SP6.seq:::::::::::::

ATACTCAAGCTTCCTTTGACCGAAGCGGTCCACCGCACCGTGAGATTGGTGGCGCCATTCGTCGTGGTGTAGCTGCTG  
TTGGCGCGCTCGCCGCTATTGTGCGGGCCAGCCTTGTGCGGGGCGCCTTCTACCCACAAGTCGGCACTTCCGCAACCG  
CCCAGCTCGACCGCGAATTACGGCGGCGCAACGGCGCGCGGAAGGCGTCACGCAATCGCTTATCCTTTCCAGGTTC  
CAATTCCTCCGCTTACTTGGGTCTTCATCGG

:::::::::::::Rv225T7.seq:::::::::::::

GGCAGCGGCGACAACCGGAACGTCGCGACCGTGCTCAATCACGGGTGCACGGTGTGCATCAGAATGGCGGGGTTCGT  
GTGCGCGGTGAGGCGTTTCGGCAGGAGGTAGTGTCTACCCCTTGGCCGCGGGTTCGTGCGGACTGAAAGGGATTTTCA  
TGGGAACCCACGGCTGCGTATCGCAGGGCTCGGTGACGTCTGCTTCTCNAGCTCAGGAAGTTCGGCGAGAATCTCG  
GTGGATGTTATTGGTCCGCTAC

Clone Rv226

:::::::::::::Rv226SP6.seq:::::::::::::

ATACTCAAGCTTTCTCGGCTTCTGTATAGCCTGAGAAGAACCCCAAGTTAATCCGCTGCTTCACTATTCTCCAGC  
GCGGGTATTCTTCTCGCTTCCGGGCTGTATCATATAACTGTGCAATGGCGATAGCCTTCGTATTATCATGACCA  
CGTTTATGCACTGGTTAAGTGTTCATGAGTTTCATTCTGAACATCCTTTATTATTGTTTGGCTT

Clone Rv227

:::::::::::::Rv227SP6.seq:::::::::::::

ATACTCAAGCTTGGTGACCGCGACCGGATACGTTGCGGCAGGCATCTGGGCTGGCGGTGGTTGCGCGCTCCGAAGCC  
TGCGAACACCATCGCCAGCGCGGCTTCCACATCAACGACCATTTGCGGCACGTTGCGGCGCATCAGCGGCTTGTGAT  
GAGCGCCACCGAATGCCCCCGGCTGCGCGGCTATCATCGATTTCAGCATCGCGGCGCGGCTTGGCGAGGGC  
GAACGAGGCGGTGCCAACCCGAATCTGTTTGGTCAGCTCCCTCATGCGGTTGATTCTTGCCTCGCGACGGGCGC  
GCGTCATGCGCTGGTTGCGC

:::::::::::::Rv227T7.seq:::::::::::::

CCGTTGCGCAGCGTGAGCGGATAGTTGACATCCGGCTCGGTGAAGGTGAAATCGATGGCCAGGTGAGGTCCCATGCG  
CGTGGGCCATTGATGCTGATCGCCAGGACGTCAAGATTGGTCCGCGCTCAGCTGGGCGAAAACGTGGGCGCGGG  
ACTTGCCTCGGAGCTGCCCGGTTCCGTCGCGCAGCTCGCGCGGCCCGGTGAGAAAGAAATTCGCCGAGCTCGCACAC  
TCCGCGCGTAGGCGCAGCTGCTCCAGGGTGTGGCATAGAGCCCGGCGCGGCGGCTGCTCGCTGTCGCGGTCGCGGACAC  
GCATGCTGAGAACGCTTGCCGCCAACGGGAAATCACCTGCGTCGAAAGCTTCCGCGGCGACGCTCAGCACTCGGTC  
GATGCCACCCAACCGCT

Clone Rv228

:::::::::::::Rv228SP6.seq:::::::::::::

ATACTCAAGCTTGGGATGTTATCCCTTGACGCGTGAACTATGTGTAACACACCGGCACCGGAACGGTGTGGGGGAC  
CCCATCGAGTTCGAGTCTGCTGCGGGCCACTTATGGCTGGGTAAAGGCCAGGCGAGAGCCCGTGGCGATTGGGGTCTG  
GTCAAAACCAACATTCGGCCACTTGTCCAGGGTGTGGCGGCGCGCGGTGTGGCTGGATTATCAAGAGCGGTGCTGGCGGTGCAAGGT  
GGGCATATTCGCCCACTTGCATTTACCCGGTGAACCCGCGCATCAACAGCTCGGCGACGCGGCTGTTCTGTGCGG  
ACCGAAGCGCCCGCTGGCGGCGCGGTGCGGCTGCAACGAGGCTGCGGTGATCGTTGCGGCTCAGCGGGACCA

:::::::::::::Rv228T7.seq:::::::::::::

CCGCTAACAGATCAGCTCGTCGACCTCACTGCCGGGGGTGAATCCCCACCGGTGCTGCGCGCTGCCAGTAGTGCA  
CCTTCTTGACGCGCTCGAAAGGGAGTCCGTGCGGTAGGTCAACGTCAGGAGCCGCTACCCAGGTGGGCGCGGTGAC  
CGGCTCTCTCGAGTATCTCCGCAACGCCGCCACCGGTGCGGCTCTCGCCCGGATCCACTTTGCCCTTGGGCAAGCACC  
AGTCGTGCTGAACGGGGCGGTGAATGACAGCGATCTGCACGGGCCCTTCCAATCGGACTGCCGGGTGCCAGAAC  
CCGCAACCGCGCGCTACACAATTCGGGCCGCGGAGCGCGCGGCGGCGAGANTTCTGGATCGACACCTCAACTCTGT  
CAGGTCAATTGCGCAAGCTGCTCGCGGTGTTGGATGTGTTG

## Clone Rv229

:::Rv229SP6.seq:::~

ATACCTAAGCTTGTATGCCGCCGAAGCCAGCGTGAGCAGCGCCGCCACCACGCGGGGTCGGGCGCGGGGCCG  
GCCGCGAGCTGCTCCGCTCGGTGATGGACGCCACCGCCGACACCACCGGCTCGCTACGTCGAGGCATTACCGGGCG  
GAGCTACATCGCTCGCGGCCAGTGTTCGGGCCCTCTTTCGAGGTCGAGGCTATACCGATTTCGCATCCGCAGC  
CGCACCTGTCGTCTGTCGCTGCCCTACCTCTGTTGTCGGCGGGGCCA

:::Rv229T7.seq:::~

TCCGTACGGCCCGGTTACGCTTCGGTCGAGTGTGCGAGTGATAGTACGACCCGGGACCTCGTCGGCATCTTCCATA  
GCCCGCCACACCTTCAGTTGCTCACCGGAATCCAACCGGTAGAAAGTCGGCGAGCGCTCGGCATTGGTCATCGGGATA  
TGCCGCTCGGGACGCTCAGAGCCCTCGGGTCCGGCCAGCACTCCGCAGGCTTCGTGGGGTGGTCGCACGCGCATGG  
GCCACCATCCATCCACAGGCTCTGCGCGAATCACCCG

## Clone Rv22

:::Rv22SP6.seq:::~

GGACACATTCGGAACATTGATGACAAAATAGAAATCATTGATGGTTGAGTCACAGGCCGATCAAGCCTTCGCCGAG  
CCAAATTCCTAATCAAGAGGCCCAAGCCGCTACCAATCAGCCCGGCAACGAGGGATTCCGTTCATTATCAGCCAAATAA  
CTGCTCTCGGGTTACACCCAAACAGCGCAATATGCGGAAAACGGTCGCCGTTGCACGACATTAATGTACCGTATT  
GTAAATTAAGAAGATACCCACCAAGGCAATCAAATCAGAGCGGTTAAATGACCGTAAAGCGTCGCTCATCTG  
TTTGACCGTGTCCCGTGGGTNTCCGAGCTTTCATACGCAACCGGCCGCGAGTCTTTGTGGATGCGTGTGTCAGT  
GGCCTCATCTTTGATGATCA

:::Rv22T7.seq:::~

GCCTGGCCGAGGTGAAGCCGCACTCGACGCGAAAGCCGCTGATCCGGCAGATGAGTCGGTGGACTGGGACTTGAAT  
CGCTGCGATGGGCGTGAAGCCGAGCCAAAGATGACGTGGCGCGCTGGTGGGCCGAGAATTCCAAGGAGTGCTACTCGT  
CGGGTTGGCCGATCTGGCCAGGGCCTGGCTAATTGGAAGCTGGCAAGAACGGGACCCGAAAGGCCGGCGGGTGG  
GCTTCCCGGATTCAAATCCGGGCGCGCTGATCCTGGCAGGTCGGGTTACACACCGGCACCATGCGCATAGAGGATG  
ACCGGCCGACGATCAGCGTCCCGGTGATCGGGCCGCTCGCGGCCAAGGAGAACACCGCCGGGTGCAACGCCACCTCG  
TGAGCGGGCGCGCGAGATCCTGAACATGACCTTGTGCGACGCGTGGG

## Clone Rv230

:::Rv230SP6.seq:::~

TAACCTCAAGCTTCAAGTCCGNGTCCGACCCTGTTGACGCGCTACCTGAATCAACCCGATGCCCGCCGCGGCGTTG  
ACCCGACAGCTGATACCGCACCGGCGACGTCGCGGTGGTTCGACGGCAGTGGGATCGACCGCATCGTGGGACGCGAGTC  
GGTCGACTTATCAAGTCGGGTGGATACCGGGTCGCGCGCGGTGAAATTGAACAGCTGCTGCTCGGGCATCCGGACGT  
GGCGGANGCGGACGTCTCGGGTGTCTGCACTATTATCTAGGCCACGGGATCGTTGCCTACGTAGTCGGCTCAGCGAA  
TGTGATGCGGACGGGCTTATCAACTTTGTTGCCAACAACTTT

:::Rv230T7.seq:::~

CCATGTCCGCCAACATATCGTCGATGTTTCGCGTCGTCGCGCTCGCGCAGTGGTCTGTCCAGGTCACGTTAAACGCC  
GCCGACATCTCTCGCGCGGCGGCAAAACGTGAAAACGAGCGGGGCGACTGCAATTGTATGACACCGACCGCCCGCA  
TGCGCCAGGCTCTGGCAGATTGCTATCTGTGCGGCCAGTGCACGACGCGTCGCTGATACGCGCGGCGGACGAGT  
TGAACGACATGGGATCGCTCGCGCTCGAAAGTCCCAACGCCACACCGGCCGCGGGCTGGCCGCTCAGATTCCANACT  
TGAAAGTACTGAAGCCGCTGCACCAAG

## Clone Rv231

:::Rv231SP6.seq:::~

CGAAAGCGTGAACAGCTCGCGGCGAGCCCGACGTCGTCGCTCGGATAGCCGCGGGCGGAAGATCAATTCCAGCGAG  
CTCCCGGACAAATCGGCTCTGCTGGCCCGCAACGAGGACTCGAGGTCACCCCGGTCGCCGGGTCGTGGTGCACTG  
CCGATCGCACAGGTTGGCCCAACCGCGCGCTTGATGCCCGGTCGCGCAAGCCCGGCGAGTTGCCAAACCCAGCGTGT  
CNTGCTCNGTCTNTANTTTCGGGAAGAAGTGGCTCGCTGATCACTACCATCGGCCAGGATCTGCGTGTATCACA  
ACGCTCGCCAAAGAGGTTGTTGTG

:::Rv231T7.seq:::~

TCGCGCACGCTTCGCGCGCCGCCATACGCGCGCTACCGATCTCCGCGTCATACACCGCGGTAATCGCCGACGGTG  
CCGGTTCGCGAGCCGAAGGTGAGCAGCTGATTGATCGAGTTCAGGTCACCGGTCGCCGGGTCGTGGTGCACTG  
TCAACGACGTCATACGTTGTGCTTTCTACGCTCACGACCCGGTGACCGTAGTCGCCCGGTGCGCTCGGCCGAGA  
AGCTGCACCGCACACCGCGACAGCTCTTGACGCGGAGCCACCCCGGATCGGTTGTTGCCAAGGTAATTGGGTC  
ATTTCATTGACGGGACGCCAGCC

## Clone Rv232

::::::::::::Rv232SP6.seq::::::::::::  
CATTCTTTAAACAGTTGTTTTGGGCTCGGCATGGTTAGCCAACTTCTCGGGTCCACCATATCATCTTGGTCCGGTAGC  
GCTCGTCCGGGTATGCTGCCGCCGGGATTCTCGCTGCTATTACTCCCCCGAAGAACCGCCACCGGTCCAGCGCGTG  
GGCCGNCGGGTCCCACTCAACAACTGAACCCCAACAGGGACATGCTTATCGGTAGGGCGCGGCCAAGGCGGGACGA  
ATCGCATCACTGCGCTCTGCGGCTCACTATTAACCCACCCGGACTTCACTTCCACCACCCCGAATGGCGCCGGTCTAT  
TGATCATCTGGCGACCGCGGATAA

::::::::::::Rv232TT7.seq::::::::::::  
CGGTGTCCTGCAAGTTGTTAGGCTCGACTTTGTGCATCATGCCGATGCCGGCGGCTCGTGGCCACGCATGTACAGCAC  
CACGCCCGCCCCCTCAGGCGCGAATCATGCCAGCGCGGCTCCAGCTGAAGCCCGCAATCGCAGCGGCTGACCAAAAC  
ACATCGCGGTCAAGCACTCCGAATGCACCGGACAGCACCTCGTCAACGTCGGCGTTGGGCCCGCGCATCTCGCCGC  
GGACCATGGCGGACATGTTCCAGCTCTCTGTANATGCTGTGTAGCGGATGGCGGAAACTCCCCATGACGAGTCGGA  
ATCCGCGCCTCGCGGACCCGCTCAATGTGCT

## Clone Rv233

::::::::::::Rv233SP6.seq::::::::::::  
CGGCATCTGGCGGCTGAACCTGTCTTGGGCAACATGCCGAGGATCGCCTCTTCCACCACGCGGTTCGGGTGGCGTTG  
CATTAACCTACCGATGGTGGCGCTTGTGCAGGCGCGCGGATACCCGAGTGC CGGTAAACCATCTTGTGCTGCAGTTT  
GTCCGCGCTGATGGCGACCTTGTGCGGCTTGATCACGATNACNAATCACCGCCANCAGACATTTGGGGGCAACCTCGCG  
CTGTGCTTGGCCGCGCAGCAGGCTTGGCCGCCGCGACGCAAGGCGCGCAACACACGTCCTCGTGGCGTTCGATGACGTACCA  
CCATCGCGTGGTGTACCCGCCCTTGGG

::::::::::::Rv233T7.seq::::::::::::  
CGCGCAAAATGAAGCACTNTGGCCACTNCCGCGGGAGGGACAATCTCGGCGGGCTAGGGCTTCTCGCGGGAAGG  
CCCGAAGCTACTGCGTTTCAACACGTCGCGTCCGCCCTCCGACCGCGCAACATCTTGGGATGGCAGCAACCTGTTAGCAC  
CTTGCGCGGGCGATGATCTCAGCGTCGCCCGGGTGTGCCCCCGGGCGGCTACAGTCTGAAACGCGATGACCATC  
GATGTGTGAAGCGCCGATCCGACNCAACGGTTCTACACTGTGATATGTCGCTCGCTGCGCGGTGGACGCTGGGT  
CTATCCCGGA

## Clone Rv234

::::::::::::Rv234SP6.seq::::::::::::  
CGCGTTGAAGTGAAGGGGTCGCCCGGCTCGAGCAGGCAAGCCATTGTTCGATGCGGTTACCGAAGATCTCTTCGG  
TGACTGCCCGCGCGCGCCAGCTCGGCTCAGTGTCCGCGTGTGTCGCCGCGCGCACAATCTTGGCGTCCACGGTGTG  
CGGGGTGATGCCCGCGAGCAGGATTGGCGAGCGGNCGTGACCGGGGTGAATCTCGTAAGAGCTGACGCTGCGGTTG  
GGGAGGCGAATCATGGTCGTCGCTAGCTCGACTAGGCCCGG

::::::::::::Rv234T7.seq::::::::::::  
TGACAACGCGGCGCGATTACCCCGCTACCGCAGCAGCATGACCGGTAGCGAAACCCGCGGATGACGCGCAGGTGC  
GTCGATGTGCTCACGGAATCGCCCCGGCACCGGATCTCGAGGATCACCAAGTGCACCCCTCGAGCGCGACACCGAC  
GATTCCGTAACCGCCACGCGCATCGGCCCTGGGCCAGCTGATTGGAGCTGGGCTATATGGCGGCGATGGTGACGAT  
GTCATCGCTCTTACATTGTGGCGCCAGAACACCGGCTTGGGCGCGGTCGATGAACACTAGGCGACCANATCC  
CCGGGGTCAACAGGTTGACCATCC

## Clone Rv235

::::::::::::Rv235SP6.seq::::::::::::  
CGCGGACATCCCGAAGCAGGACAGCGACCGCTTCGGTGTGATGATATCAGGGCTCGCACCACGCGCAACCGCTTCC  
GGCTACCTAGACCGGCT

::::::::::::Rv235T7.seq::::::::::::  
GCATGCGGGTGATGCGGTTCTCAGTGCAGAACAGCGCTTCGACGCGGCATACCGACCGCATGCGGTGACACCGGNN  
GCCGGGCGGGAATCT

## Clone Rv237

::::::::::::Rv237SP6.seq::::::::::::  
CTCAAGCTTCAGNCNTCTAAGCGGTGTCGCGGCGATCGCAAAGATCGCCCTTTGCCGCGTGGGGGCTTGTGCTC  
GGGGGTGTTGTACACCTTCTCGAACCTCGCGACCGACACCAACCGCTCGGCTTGAACACCGCCACATCGGCGACG

ANATCTTGTATGTCCTGGTGAATCCACGGTGACTTTGGAGTGGAGGCGGCCATACTGATCGCGCGGCCACCATGAGCTAGCGGCAGGAAACACGACGCGCTCACCTTTCGCGAGCAGCGTCGGGTGATATGCTGGCGCC

.....Rv237T7.seq:.....

AGTCGAANGTCAGTCCGGGTCTCTCCGACTACGGCCAAGAACTGGGGCAGCGGTGTCAGTGCAGAACACGGGAACTGGTGGCGCCCTAGCGGAGCGAACGCTCACAAACGGCGGTGACCGCTTCTGGTCGTGCACCTGAGCCGTGCCCAGCCGGCGCGGTGGCTCAGCGCATCCACTGGATGCCCTTTCGGCGGGTTCAATCANGTACAGGCGACGTTGCCACCATCGTGGCGGGCAGGTTAGCGAGAAACGCCGACTTCAACGATTGCCCTCGGTGATGxxxx

Clone Rv23

.....Rv237T7.seq:.....

AGCTTCGCGCGCTGGCGATCGCGTTCAAGCGCGCTCTTCGAGCACACGAGCGAAGACAGCTCGGCGACGGAGCTTTATCGACATCGGTCGGGCTGGCTGACCGCGCGGGAAGAACTGCTGGACCGCTTGTTCGACGGTGCCGTGGCGAGCCGAGCGCGCTCAGATGTGACCGGGTGGTCGATGTGCCCGCGGTGGTGAGTTTCAACGACCTGACCATCGAAGATCCGCCGCATCCGAGCTGGCGCGGATGCCCGCGGTCAACGACATCTACGGCGCGGAACTGGGTGAGCCCTTACCAACGCCGGGCTGTGCTACTACCGCGACGGCTCTGACAGCGTCGCTGGCATGGCGACACCATTTGGTCGGCGACGACTGAGGACATATGTTGGCGATGTCAGCCTCGCGCCACCGCGCTCTTCGCGCTGCGGCGCGGTG

Clone Rv240

.....Rv240SP6.seq:.....

AGCTTCAGCTGATACTCGACCAGCCCCACTCGGGCCAATAGTGAATGTCTAGCATCTTACCCTTTCAGGGCTANTCGAGTAGTAGACATTGATTAGCTGAACGTACTCCGACGCCAGCTGACGAACGGGATGACGGATGGATTTCGTGTTGTCGCGCGAGGTCAATCGTTACGGATGTATCTCGGGCGCGATCGGGCCGATGTTGGCGGCCGCGCGCGCTGGCAGCGATATCCGAGAACTGGCGGTGGCGCGCTGTGTTTGGGTGGTGACCTCGGGCTGGCGGATCGCGGTGGGACGCCGCGCGCGGTGCGATGGCNCGCTAGATCATCGGCTCACGCGGATG

.....Rv240T7.seq:.....

CTGGTCATGAGCGTTGCTCGGTAAGTGCTCACTGCCGATCCTCCTCGTGAAGTGCCACCTCAGGTTGGGTAGGGTTGGGTACTCGAAACCAAGTTACCCACAGTAACACCGCTCAAAATATATCCGTTGCATAGTCAATGCAAGTTGATGTGAGCTACATTGCACCAACTAACTAACCAACCGGTTGGGTTAGCGGTGATCCTGGCCGTGTCGGTCTCTCACTGCGGTGATAGCGATCAATGAAGATATGCGGATCTAGGCGCGGACGCGCTGGCANCGTAGATCATCGGCTCACGCGGATGCGGCTCTTGGTACGGACATGCGCGG

Clone Rv241

.....Rv241SP6.seq:.....

CTCGTAGTAGCACCCCTGTAAATTTGGGATCGGCAAAAGGCGAATCACCGCGTGGCCACGACACGCGGGAGGGACNATCTCGGCGGCTAGGGCTTCTCGCGGGAAGGCCCGAAGCTACGGCGTTTCAACACGTCGCGTGCCTCCGACCGCGAACATTGCGGGATGGCAGCAACCTGG

.....Rv241T7.seq:.....

GGATCAACTACCGGCCAACGTTGATTCTTGGGCGCGCTGACGCGCGAAGCACCAGCGACACATTGACGAGATGGCCAGCGCGTCCGGGCCACGATGTTGGTGCTCGCGGGCTACTCCCATGTTGGGCNCGTGATCGACATCGTACCGCGCGACCACTGCGGCGCTCGGTTTCAACAGCCGTTGCGGCCGCGAGCGACATCATCT

Clone Rv243

.....Rv243SP6.seq:.....

AGGACCGTCAGCAGCGCGACGTGCTACTCGCGAGCAGTGGGAATCGCTCTCGAGCAAAACATTACTCTGCGCGACGTTCGAGATGACCTTCTGAATGGACGGATCTACTGCGCGCGACGACCTGGACCGCGTATGCTCCGCTCCGCTCGGACGACACCGGGGACCTCTATGACCCCGACGGAGCGCTCGCGGTACTGCTGCGGTTACCGCGACGCGCGACGAGTACGCTGCGGACTCGCTGAGTCCANCTCGACGCGGTAGCGCTGCTGCTGCGGCGATGTCTGGCATCTACCGCGGTGCTCCCTTGA

.....Rv243T7.seq:.....

CGACTCTGTTGGCCACTCGGGGTGATCTTGGCGCGCCCGCTCGTGGAAACGCCAGGTCAACCGGCGGCGACCGCGGTGACGCGCGTCTGTCGCGCGCTGGTACATGGAAGTGTGACAGCAGGAGCTTGGCGTTGGGCGACGACCCGGCGGTGCGGATCGCGAGGCGTATGACGAGCGGGGCTGATGGCCACCGTACTGGATGCTCTCCGGAATCGGGGTGTGCGCGCTTTCGAGCTGCCAGCAGCGCGCGCGCGCGCTGCGATGCTGCTGCCATAAACCTTGATACCGGCGAGTCAAGNACNNGTATCCACGGTCAACC



## Clone Rv244

.....Rv244Sp6.seq:.....  
CACACGGACGGCGGTGCGGACGCAGCTGACGCGCATGTTGGTCAGCATCGCGGGCGGCTGCTGTTGTATGCCTACTT  
CGCGCCCGCGCAATGCTGGTGGCGGGCGGTGGTGGCGCTGCATGGTGGGCTGGTGCTGACCCAATCTCGAACCA  
CACCGGTGGTGCTGGTGGGTCATGGCTATGCCCTGCCATTCGCGCTGGTGTCTACN

.....Rv244T7.seq.....

CCGATATCCGAGCCGATAGCTGGCGGGCTCGGGTGGTNGCCAGCGGGCGTGCACGAAAGTGTGACCGTCATGAAACA  
GACACCACCGCGCGCGCTCGGCCGTCTCACCTGCTCGAGATCTCAGCATCCGAGCCGGTGTGATCGCGCTTTCGGC  
GTGTAGTGGGTGCGCGCCGAGCCCGGCAACGCCGGCCGACACAACCCGGAACAGGAAGTCCGGTCACCGCGCC

## Clone Rv245

```

.....Rv245SP6.seq.....

```

GCTT CAGACAAATT GATCCCTATGCACCCGGTGTG CAGCGCGATGAGTGAAGACTGCACGCACTGGCGTGAATCCGG  
CAAAACCTCTGACAAAGCAAATCAACCGGAGCTGC AAGCGAACCTGTGATCTGCATCCGCGCTGCTGCAGAAACGG  
CAGAAAGCGCTCTCGTCGGTTCATCTGCAGCGACCACTGGTGATAGCGCCATCGGCATCGGTGCGGCCACGGTGG  
AGACGACCTCCGCGNGCGCTCTGGTCACTAACCCGCGACCACTGTCTCGGCGAAGTCGTTCAACATCGGGCGCCAG  
TCTCCAAC

.....Rv245T7.seq.....

GTTTGGCGGCCCTTATGCACTAGAGGTCGTCAAATGACCCACAGCGGAAATGCCGACTATTGCGAGCCCTCCTTGCGCT  
TGCGTCGCCGAGATGGGCTCGCGGGGAACCCGATGCAGTATATGACCTCGGTTTCTTCGGGTGCTACCCGCGGCTCTTG  
TCAGGATGAGCTCCGCGCTTGGAAATTGCTCCAGCGGGCCCAATTCATCGAGCGAGATTGCTACACATGGCCGGCGGG  
ACATACCTTCAACCCTGGATCTGCTCACGACGCCCGCTGTCTGGGATCTGCTCACGGGTAAAGGAATTA

Clone Rv246

```

.....Rv246SP6.seq.....

```

CGGCACTCCTCCTTATCGTCCGCTCTGCATCGTCGCGGCGCGGTCAAGTGCAAACGCCTTCGGGGGTGGGGGTCTTG  
CGGAGCACACCGGATACGGAGCGCAACGCGTTCGCGTTGTGCGGGCAAACAAGTGTGCAAGNNCCAATGCCATGTCCAG  
CAGCTTATCAGTGTGCAACGTGCGAACGTGCGGCCTTCGCCGTCCTGAATCTCTACAAG

.....Rv246T7.seq:.....

CGCTGAAAGCCACCATTCGCGGGTCGGGCGCCGGGCTCGGGCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCG  
CGACACCACCCGGTGCCTACGTCGAGCCATACCGGGCGGAGCTACATCGGCTCGGCCGCTAGTGTTGGGNCCTC  
TTTCGAGGTCGAGGTCGA

## Clone Rv247

```

.....Rv247SP6.seq.....

```

TGTAATTGGGATGGGCCAAAAGCAAACACCGCGTGGCCACAAACGGGGGAGGGACAATCTCGGGCGGCTAGGGCT  
TCTCGCGGGAAGCCCGAAACGTACGGCGTTTCAACACGTCGCGTCGCCTCCGACGCGAAATTCGGG

```

.....Rv247T7.seq.....

```

CTTGGGCAACATGCTGAGGATCGCCTTTTCCACCACGGGTGGGGTGGCGTTGCATTAGCTCACCAGTGGTGCCTTG  
TTGCAGGCCGCCGGATACCCGAGTGCCGGTAAACCATCTTGTGCTGCAGTTTGTCCCGCTGATGGCGACCTTGTGCG  
TTTGATCACGATGACGAAGTACCGCCATCGACATTGGGGGCGAACTCGGCTTGTGCTTG

## Clone Rv249

```

.....Rv249SP6.seq.....

```

GCATGCTTCATTATCTAATCTCCAGCGTGGTTTAAATCAGACGATCGAAAATTCATGCAGACGGTCCCAATAGAAAG  
ACATTCTCCAGGCACCAAGTTGAAGAGGTTGATCAATGGTCTGTTCAAAAACAAGTCTCATCCGGATTGAACCTTTACC  
AACTTCATCCGTTTCATGTACAACATTTTGAAGAACATGCTTC

## Clone Rv24

```

:::Rv24SP6.seq:::

```

ATATCTCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCAGCCACGCGGGTTCGGGCGCCGGGCCCGG  
GCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACCAACCGGCTGCGCTACGCTCTATCCATACGGGCG  
GAGCTACATCGGCTCGGCCGCCATTGTCNGGCCCTCTTTCGAGGTCGAGGCTATACCGATTTCGCGCATCCG

.....Rv24T7.seq.....  
TCCGTACTGGTCCGGTAGCCTTCGGTCCGAGTGTGCGAGTGATAGATGACGACCCGGGACCTCGTCGGCATCTTCCATA  
GCCCGCCACACCTTCAGTTGCTCACCAGGAATCCAACCGGTAGAAGGTGCGCGAGCGCTCGGCATTTGGTCATCGGGATA  
TGCCGCTCGGGACGGTCAGAACCTCGGGTCCG

## Clone Rv251

.....Rv251SP6.seq.....  
GTTCTCGCACGATTTCCGATTAGCGGGATGGTCTCAATTGGGTATGCGGGGAAGGCGCTGACATTCGCGCGATTAGC  
TGTTTGATGGACCGGGGTGATTTTGATCAGCGAAATGGGTGTTATNACAGTCGACGCTTTCATCCGGGCGGGAA  
CG

.....Rv251T7.seq.....  
GGGTGTGCTGCTGTGTATGCACGGCATACGGACATCCTTCCCCTGAAGACCCGCGGTGGAACAGCCACGTTCCATC  
ATCANGGGGTCAACCCCGGCCAAGGGCGACGGCACGCCAAGTTGCGCGACCGTTAACTATAGTGCTGTTAGCTTCATTT  
GCTGCGAGCAAAACAGCTGGTCCGNCGTAGGAATGAATTGAACTCAACCGATTGTTGGTCCGCGCTAGGTGTCTCTGG  
CTG

## Clone Rv252

.....Rv252T7.seq.....  
ACTACCCGGCCACCGGTGATNTCTTGGCCGCGCTGACNCGCGGAACGACGCCAGCGACCCACATTACGACAGATGGCCA  
GCGCGTGCCGGGCCACAGANTTGGTGCTCGCGCGCTACTCCANGGTGCGGNCGTGATCGACATCNTCACCGCCGAC  
CACTGCCGGCCTCGGGTTCACGACCGTTGCCGCCCGCAGCGACGATCACATCGCTTTTATTNNNTTNCNGAAT  
CCCTCGGCCCGCCTGGCGGGCTGATGA

## Clone Rv253

.....Rv253SP6.seq.....  
ACGTCCGGANACTGTTCCGCTCATCTCGTCTCGGCGGATTGGTCTGCTGCGCCGGACCGACCGATCTTCAGCGGGG  
GGTACCGTCCGTGGGGTGCCGTTACTTCCGATCGCCCAAGTGTGCGCGTGTGCTGGCTGATGCTGAAGCTCACCGCGT  
TGANTTGATCGGTTCCGGATCTGGCTGGTGGCCGGAACGONATTATGTGCTACGGGCGCCGGC

.....Rv253T7.seq.....  
GCTCAAAAGCACTACTGGCACCAGGCCCCACAGTCACCTGTGACTCCTGCGCGACCCGCCCGAGGTCTGGCCGTTA  
CACCGAACGGCGAGCGGGGAGTTGGTACCATCGAACAGACAAGGTGCATGGCGGAGTTGTTCCGCCACTTCGTCG  
ATGACGGGTG

## Clone Rv254

.....Rv254SP6.seq.....  
CGATACCGGCTGCTTACCAGACATCCACCATGCCACCCGAATCACCGCACGCGCCGAAATCGCACAAACAGTTGACG  
CCTTGACGTTTCCGCGATTGGAATTGCCGACGGTCTCTGACGGCGTCGACCTTGGCAGCCTCTACGAGCTCTCGGAAT  
CACTTGCCACGAGGGGGTTCGATGAGTGTACACCGAAGACCTCGATATGGCGCAATCCTGGCCGACATCCAAAC  
CGGGTGGTTGTGTGCTGCGGGCCGGTGGGGTTCNGCAANACATACCGCGGCCGCGCTGGCCTTGCAGCGGGCCGAAT  
ATGGCCGCACTGTGGTCTG

.....Rv254T7.seq.....  
CGTCGTCGTGGTATGCGATAGCCATCCCGTGGGGTACTCGCCATCACCGATCAGCTTCGCCCGGAAGCGCCGCG  
GGCGATTTCGCGTCCGACAACTGACCGGGGCCAAACCGGTATTGCTTACCGGCGCAACCGGGCCACCGCGATCG  
GCTCGGTGACAGTTGGCATCGACGACGTACGGGCGGGCTACTGCCGACGACAAANTCGCAGCCGTGCGNCGNCTG  
CAAGCTGGAGTGCCAGATTACCGTGGTGGTGACGGTATCAACGACCTCCGGCCTTAGCGGCCGCGCATGTGCGAT  
CGCCATGGGACGCGCCGAC

## Clone Rv255

.....Rv255SP6.seq.....  
GCACGCAATCGAAGTCACCCAAACGGGCGGGCGAGGCGTCTNACGCCACGTCTNACAGCCGCAACCTCAACCCGGCC  
ACGGCGAGCTCCTGATCAGGCGCGAGGCCATCGGTGTCTACTTCATCGACACTACTTCGCGTCCGGGCAATATCCGC  
GCGAACTCCCGTTCGTCTGCTCCGAAGTATGCGGCGACGGTGGANGCCGTGCGCCAGGGGTTAC

000673476.1 (3000)

.....Rv255T7.seq:.....

TGCAGCTGTGGGCGACAGATCACGCCCGCATGCCGAGCACGAGAAATGCGTCGAATTGCCCGGGGCCGGCCGGCAT  
GCTCGGGTTGCAGACGGCATTGTCCGGTGTGGTGCATACAATGTTGGCGCCGCTTGTGANTTNGCGCGATATCGC  
GCGGGTGTAGTGAGTANAAACCGCGTGC

Clone Rv257

.....Rv257SP6.seq:.....

GAACCTGACACCCCTGGTCAAGGGTGAGCAGGACTTGATTCTTCTTCTGCTGGCGCTGTGAGCACACCAACGCC  
GCTGACGGCGCTCGCGCTCTCGCTGTGCTCGGTCTGGTGGAGCGCGCTGCCCGGGCCNACATCNTAAATCAAGCGT  
ATTCTTCAACAGATATCATCAATGTGCGCGCTGGACTATTCAAATCATCGATATACTGGTGACCTGTCTTCCGCAT  
CGATCAATGGCGATAGTCACGCAATCGTCACGGACATCGTCCGCGCTCCACGCTGCCCGCTGCCAACAGATGCTGCAA  
CCCATCGGGGTGGTATCACCGCGGTGCTCGGCGATGGTCCACAATCTTTCGCGTCCAAGCCNAAACATCCCGGGCAT  
GAATTCAACCGCATGCGCN

.....Rv257T7.seq:.....

CTATCGTACCCGCGCGGTACACTTCTGGATATCGCCGGCCTGGTCAAGGGGGCGTCCGAGGGAGCCGGGCTGGGTNA  
CAAGTTCTCTGGCTCATATCCGCGAATGCCAGCCATTGTACGGTGGTGCGGTGTTCGTCGACGACGAGCTGACTCA  
TGTCAACGGACGGGTGATCCCCAGTCCGACATTGAGGTGCTCGAGACCGAGCTGATCCTGGCAGATCTGCAAAACCTT  
GGAGCGGGCCACGGGCGCGGTGGAGAAATGAAGCGCGCACCAACAAAGCGCGCAAGCGGTCTACGAAGCGGCACTGCG  
TGCCACGANGTGTCTGACGCCGGGCAAGACGCTGTCGCCGCGGGGTGGATGCCGCCGCTTGCGCAGCTGAAACT  
GCTGACCACCAAGCCCTCTCTGT

Clone Rv258

.....Rv258SP6.seq:.....

TACTCAAGCTTCAGCGCGCCACGTCGCGCGTCCGTCCGGCGACGTGACCTCGAGCGCCGAGTTCGACTTCGACTCGCCG  
CCGCGCATGCGGCATGAAACCGGGCACTCACCGCAAGCCCGTCCGAGCTCAGGTGATCGACTCCGCTTCAAGCAC  
GGATCGTCCGGGCAACTCGCGGCTTCGCGCTGTGCGAACGGCACACCGCTCGTGGCGGCNCCCCGCGGAACTGGGC  
TCATCACGGTCGTTGCGAGCGGTTCGCGTACCCTGACCGACGCCGCT

.....Rv258T7.seq:.....

CCGACATCGAGTGGGCTCGCACTGACTTGGCGACTCCAAGCCACCGTACCCGCGCGCGGCAAGCCAAAGGACGAG  
ACGGCCTTGCCGGATAGCTGGCGCAGGCGTTCGCCCAACTGGCGTCCAGCTCGCCACGATCGTCAAGAGGCTTCATC  
TGCCGAGTGTGTCCGCATCTCATGGCTCCAAATATGGAATTAGTCCCTGGCGGACTGACGACAGTCCCTCAGCGAC  
CGAATTGCGCATCCCGCTTGTACGCTACTCCGCAAAATCCCGGGTTCGCTCCGCGGAAGCGAACTCGCGGCGCTAC  
GTGTGGTTCACTTCGGCGCTGCGCACTCGGATCGACGGCGGATGTTGGCGGGCCGCGCGCTCTTGGTCATCCG  
ATTGAGT

Clone Rv259

.....Rv259SP6.seq:.....

ATACTCAAGCTTGTCCGCGTAAACCGCACGACGGGCGGTGGGTGCGGTGTCAAAGACACCCACACTTCTTTCGCGTTC  
GGTATCTCGACACCGCGCGGAGCGGACCACTGCGCGCTAGATCGGCGATCAGCGCGTCCGGTATCCGCTGGGT  
CGCGCCACCGGAATTCGCGCAGCGACCGAATGGCGCAGCGTTGCGACGATCAGTCCGCGCGCGCGCACCAAGTGA  
GCGCAACGGTGAATTCGCTGGGCGGCAACGCGGTGAACACGCGCGGCGATCCTCGCCGCGCAACGACCGCGCAGCG  
AGGTCGCTGGGCGATCATCCGACGCCGA

.....Rv259T7.seq:.....

TGGACTATAACGATCGGGTTCGAGCAGCGCAACCAACGAGCGCGGACGAGTGGGCGAGGTCGCGCTCCCCACA  
AACAGGATCCGTTGCTTGGAGCGACAGGCTCCGTTGCGGCGTGGGCGCGTGTCTGTCACGCGTCCGTTCCCGGG  
TCCCGCGGACGCTTGTTCCTCATACTCGCCCCCTAATCTCGAGGACGCGGATACCCGAGGCAACCTCCCAAAA  
TGCAATCCCCAAAATGCAATGCTCGAGCTATTCTCACACGAGCCGCTAGTTGCGGATCAGAATCCGTTGGGCGC  
GGAAGTCAAGCGCAATTGTTCTCCCGCTCCGCACTCATGCTTGAATCGTTTGGAAATCATCCTCATATGCTCGATC  
GTTTCATAGTCAAGCCCAACCCGCGAGATGGGTGGCC

Clone Rv25

.....Rv25SP6.seq:.....

CTTTACACTTTATGCTTCCGGCTCGTATGTTGTGGAAATGTGAGCGGATAACAATTTACACAGGAAACAGCTATG  
ACCATGATTACGCCAAGCTATTAGGTGACACTATAGAACTCAAGCTTAGTGGTTGCGCACGTAATTCGTCAAGT  
GACCGATCCCTGCTGTCTCACTCGCTCACAGCGACCAACAGGCTGCGCTCAAGCGGGCAGCTGCGGAGCAGAT

GAGGAATGTGCGACGCTTTGATGCAGCCTGTGAGAACCCGAGACCCCTCGAAGAACTTACGATCGAAACCGCTTAGGC  
CAACCGGTGACGGGGTGTCTTTCCGCGCTAGGGCGCCTTATCGTCCGAAGCCCGTGGTGGTATCGCTTCTGGG  
TCGCGCTTGC GGCTGTGCTTGC GCCAGCGTGGCCTCCCTGGACCGATCTCCAGCGGCATCCAGTGGCGATTCTGCC  
ATCGG

.....:Rv25T7.seq:.....  
CAGGCATGCAAGCTTGCATGATCAACACGCGCTTGC GCGCTGAGCCGATAGTTGACATCCGGCTCGGTGAAAGT  
GAAATCGATGCGCAGSTCGAGTCCCATGCGCGTGGGCCATTGATGCTGATCGCCAGGACGTCAAAGATTGGTCCGG  
CGTCAGCTGGGCGAAACAGTGGGCGCCGGGACTTGCCCGGAGCTGCCGGGTTCCTCGCGCAAGCTCGCGGGCCCC  
GGTCAGAAAGAAATTGCGCCAGGTGCACACTCCGCGCCGTAGGCCAGCTGCTCCACGGTGTCCGCATATAGCCGCG  
GGCCGACGCTGCTGCTGTGCGCGAAACCCGATGCTCGAAGACGTTGCCGCCAACGGAAATCACTGCGTCAAAG  
CTTCGCGCGGCATCCAGCACTCCCTC

## Clone Rv260

.....:Rv260SP6.seq:.....  
ATACTCAAGCTTGACCGACGCTGATCGCACCGCACGCGGGAACCTCAAAGGCACTACTGGCAAGGGGCCACACGTC  
AACCTGTTAACCTCTGCGCCGACCGCCGGAAGTCTTGGCGTTAAACCCGAAACGGGCCAACCCGGGAATTGGGTT  
CATCAAAACAAATGACAGGTGCTTGGGCGAGTGTTT

.....:Rv260T7.seq:.....  
GTCGTCTGTGCTGGGGCGTCCGTATCAGCACGCCACGAAATGGGGCAAGAAGGATTCTCGAACGGTGGCTGTC  
CAAGATCACCCCTCGCCCAAATGCTACGGGCACTTCTACATCGAGCACAAACCCTGGCCATCACGTCCGCGGTGTC  
CACCGGAGG

## Clone Rv261

.....:Rv261SP6w.seq:.....  
ATATGCGTTGCTGAGCTTTTCGGATCGCAGCGAGTCTGACCCGCGCGGTGACCTTCGTGGATATCGCGGGCTGGTC  
AAGGGGGCGTCCGAGGAGCGGGGCTGGGTAACAAGTTCTGGCTCATATCCGCGAATCGCAGCCATTGTCAGGTG  
GTGCGGTGTTCTGTCACACACGACTGACTCATGTACCGGACGGGTGATCCCACTCCGACATTGAGGTGCTCGAG  
ACCGAGCTGATCTGCGAGATCTGCAAGCCCTGGAGCGGGCGACGGGGCGGCTNGAA

.....:Rv261T7.seq:.....  
GACACCCCTGTCACGGGTGAGCAGGACTCGATTCTTCGCTATTGGTCGGCGCTGTTGAGGCAAGCACCGCGCTGAG  
CGCGTCGGCTCTCGCTGTGCTGCTGCTGGTGGAGCGCGCTGCCGCGGGCCGAACATCGTAAATCAAGCGTATTCTGTC  
AACAGATATCATCAATGTGCGCGCTGGACTATTCAAATCATCGATATACCTGTTGACTCTGGTCTTCGCCATCGATCAA  
TGGCATAGTACGCGAGATCTGACGAGCATCGTCTGCTGCCAGCTGGGCCGTGCCAACAGATGCTGCAACCCATCG  
GGGTGATATCNC CGGGTGTCTGCGCGATGGTCCAACAATCTTTCGCGTCCAAGCCCGAAACCATCCGGCCATGAGTTC  
ACCGCATGGCGCAACGGCTGTTGCCGGGCAAAACGGGCGCGATCGAATTC

## Clone Rv262

.....:Rv262SP6.seq:.....  
TGTAGAAGTGGGTCCCGTCCAACCTTCGCGCGCGCGCGGATATGCTTGTGCTGCTCATTGATATCCAATC  
TATGGGTGCTGTTACTCAACGGGCGAAGCTTGGCCCTCCACGGGTAGGCTCTATTTCAGCGGTGATGTCC

.....:Rv262T7.seq:.....  
CCCGAATCCGTTGGCGCGGAGGGGCTTGGCGAGCTGGACACTTCTAACTTGTCTTTACCGGTCACTGTTGCAACCC  
AACACCTTTAAACGACGTGACGACGCTTACATCGGATTCAGCGGTGTCACACAGCGTTGCCATTGGGACACCCAC  
TACGCCAAATTTCTCCGACTGGGACACCTACCGCAGCTCGCCCCACTGCAGGAGTGTGTTGCCGCAACGGGCCATC  
GACATGATCCAGTCTGTGTGACCGACGCGGAGCAGACTGTTGCGTATCCGCGTTGGGCGCTGGCGAAATTCGCCAC  
CGCATGAT

## Clone Rv263

.....:Rv263SP6.seq:.....  
TTGAGATGCTGGTCGGGATGCCGATGTTTGAACATGTCCTGGCGTGAATAACGCGAGCGCATGAGCTCACCG  
GTTCCGAACCAAGTATCGAAGAACTCGCACTGCTGGCAGATGSTATCTCCGATGGTTGTAATTTGATCCCAACTC  
TAACTGTGCTATCGGATTCGCTGAATA

.....Rv263T7.seq:.....  
CGTATACAGGATCCCGCTGAGACACTTGACCTTACGGCCGAAGTGAAGTTCGCTGCTGCTATGCCGACACCCGATTTC  
ATACGCTGCTGTACACGACGCGCGGGCGGTGGCTCCATCACGCTCAACCGCCCGGAACAGCTCAACACCATCGTCC  
CGCCCATGCCGACGAGATCGAGGCGCGCTATCGGGTTGGTGAACGCGACAGGACATCAAGGTATCNTNCTGCGCG  
GTGGCGGGCGCGCTTCTCCGGCGG

## Clone Rv264

.....Rv264SP6.seq:.....  
CAAGCTTAAGCTGTTCCGGCCACTCCATGAGCCGTAGTGCAATGGTTCGTGCACGGCGAGGCCGAACCTGCCATAAA  
CATCCCTGACGAAAGTCTCCGGCAAGCCGATTGCTTCTTCGGGCGGCTTCTTGTGGATTGTCCGATAACCCGGTCCCT  
CATGTGGGAAGTTGTGCGCACTCTTTCCTCCGCGATGTGGGCTAACGACTCGCTATTGAGCAAGAAGTACGTGCACA  
GGCATCTGTCGGCGGGGCTTCAACGACGCGGGAGATCTCGTCCAGATAGTGCTCCACGTCGGGNGGAAACATGTGGGTG  
AACACCGAGGTNAGAAACACNCATCCAACGACGATCCGGGATATGGAAAGCGAAA

.....Rv264T7.seq:.....  
TATGGCTTCGTGCAGCACTACGCTGATAGCGCCATGAGCCAGCGACTGAAGCGCGCCATGCCTGCACGGGCCGCTC  
ATCAGCGAGGCGGCCATCTCCGCGAGATAGCTTCCGCGCTCGGCGGCGACGCTGCGGATCGCGTCCGAGCTCGCT  
GACGCGGCGACGCGCGCTCGTCATACCATCGGCGATCCAGCAGTTGGGTAACTCAACGGGGTCCGTCGCTAGCGG  
CGTCAATTGATTACGACAATAACGATCGCTGCAGCAACTTTCGAGTCCGATGCGGGCCACTCCCGTGCAGTCA  
TGGCTAGCCCCGCTATGCCGGTTGTGTCGATGGCAGCGACGGGCTCGTAACTGCGGCTCAGCTCGCTGG

## Clone Rv265

.....Rv265SP6.seq:.....  
GCTTAGCGGTCTTGCTCAACCCGACATTGCGTGCCACTCATGAGCGGGTGGCGGTGCGGCTGCTTACACATCT

.....Rv265T7.seq:.....  
GTATCTGGCGCTCTCGAATATCCTTGAACGTCCGCGGTGCCACCCAGATAGATCGCAGCGCCCTGCAATGGAATT  
CCTTTATGGCTCTCTAGCCTCCCGCTTGATCGGCTCGACCCGAGAGATGCCCTCGGGGCTTGGGGATCTCCCTCCA

## Clone Rv266

.....Rv266SP6.seq:.....  
CTTCAGCGGATCCGCGACCGCAACGCGACGGTGACGGTGGGCGACAAGTTTCGGTTGGTGCCTCGCGCGGCTGGGCG  
ATATCAGCTCACCCGTTTCGAGGTGTTCGGCGACCGGAGGCTGCTGCAGACATTCTTGAGCGTCTCGACCGGCGCG  
ATTTCGGCTTCAACATCTGTGACGCCGTAATTCGGCGGTACCGCTCGGCGCGGATCGAAGGCGGCCCTGAGCTAAAGCC  
GGCATCTGCGGAGTGGTAAACAAGTTTCGGTGACTTCGGTTGACCGACTCGACGGGCTCGATCTGGGCGCGCTGGACC  
GGTATCTCGGTTTCGCTGGGGATCGGGCCNACCNCNANTTGGCTTGGCANCTGATTCCGGTGGAGCTCCAATCTGACTT  
CCGG

.....Rv266T7.seq:.....  
GCAGCTACCGACCTAGCGAGAGTGTGTTTCGAGCGTCGAATGTGAACGTTTCGGCGTGATTTCGGCGCGGGTTC  
GCTCTCAGCGCAGCTTCCGCGCGGAGNGGCTAGTCCCTGGTTAAGCAATGTCTCGGTGCGCGGCAAGCGCGCATG  
TCGCCAACCCGTCNACCGCGTTGGCGATTCGCGTACCGACGGAACGACGGCGCGATCCGGATGTTCTGTGTCGCG  
GATCCTTTGATACGGGAACGACCCCGCTCGGTACCGCGATACCAACGCTCTTAGCCAANGCTACNGTCCGGCG  
CGCGGTCCGGGCAACACGTCGAAGCTGATGAANTAACACCCCTTGGGCTCGGTCCAANGCGATCTTGACTCCTT  
AACCGCTGATNCAA

## Clone Rv267

.....Rv267IS108IN60.seq:.....  
TCCCCATCGGGCGGAGCTGTTAAAGTCCAAGCACGGGTGGGATGGAATCGACGACAGTTGAGCGCGCTCGGTGGC  
CGTGGTCAGCAGCTGTGTCGGAAGCGCACAGGTACATCCCTCGACATCTCACCGAGTGGCACGGGCGACATCAAC  
AGGAAGATTGACGAATCCCTCGCAGGCGGGCACGCTCGCAGGCGCAAGCCCACTACGGGCGCACCGGATCTCCG  
CTCAGCAACGCGCAAGCGAGGCTCANCCACCAAGTCGGGCGCGCTCTCCCTCGCCCTGGTCTCCGGGCGCTT  
GTTAAACACTACCGGAAGTCCACCAATCTCGTGCATCTCGACACCGTCCGCTCTACTCCCTCTCTCCGCGCCCTC  
TCCACACNACACCTCTTGCAATTAAGTACGGGACGGTCACTTTTCGTCGGACGAAATTCGAATCCGCGCGCTCG  
CCGCCAGAGAT

.....Rv267SP6.seq:.....



:::::::::::::Rv270SP6.seq:::::::::::::  
GGCATCTTGGCGCCATGTTAGCCCACTGCCACCGGCTATAGAAGCGATGCGCACCGTCTGCCAGCATTGCGGC  
GCTCCTCCCTGGAAGCAAGATAACCAAGCTCATGCCGTGGTTGTGGTGGCGTGTTTGGTTTGGTAACTTTGG

:::::::::::::Rv270T7T.seq:::::::::::::  
TCGGCTAATAATCGTCGAGCGCGGGCTCTCTCGAATCGCTTCGGCGGTGCGCGGGTTGTACCGGTGATCATCACGG  
GCTTATCGACNTCCGTTCCGGCTGGCTGACGGCGGCNAATAATGCTGGACTCGTTGTTGTGACGGTGCGGTGGC  
CGATGGCCCGCGCGCTGCTGTTATCGGTCATTCCGCAACGACTAGGGGTGTCCCGCGCGGAGCTGATGCCCTCGAC  
AATGGCACCCACTCTCTCGGTGGGTGGGCACCGTGATCGCAACCCACTTCATACCCGACGCGCGGCACCTTGGCG  
ATTGACGGATG

Clone Rv271

:::::::::::::Rv271SP6.seq:::::::::::::  
CTCAAGCTTGGAGGCGTGGCGATCGCGGTCCAAGGCGCGCTCTCCGAGCACAACGAGCGAAGACNGCTCGGCGACGGA  
GCCTTTATCGACNTCCGTTCCGGCTGGCTGACGGCGGCNAATAATGCTGGACTCGTTGTTGTGACGGTGCGGTGGC  
GAGCCGAGCGCGCTCAGATGTACGACCGGGTGGTCTATGTGCGCGGTTGGTGAGTTTCCACGACCTGACCATCGAAG  
ATCCGCGCATCCGCTGCTGGCGGGATGCGCGGTGGCTCAACTAATTCTACGGCGGCGAAGTGGTNATCCCTTCN  
CCACCTCGG

:::::::::::::Rv271T7.seq:::::::::::::  
CCTAGTCAACCGTACCGCTCATCGGATCGGGGTGACCGCACAGATGGAAGTGGAGCTTCGGCGAGGTGATCGCCTATG  
CCTCGCGGGGGTGAACCTGACCCCGGGTGACGTGTTCCGGCTCGGGCAGCGTGCCCACTGACGCTCGTGAAGCAC  
CTCAGGCCACCGGAATCATTCCCGGGCTGGCTGCACGACTGCGAGCTGGTCAACCTCCAGGTGGAAGGGCTGGGCGA  
GACGATGCGAGCCGTCCGACGAGCGGCACTCCTTTCCGTTGGCTCTTCGGCGGAATCCGGACCGCGAACCAGCG  
GCGCGGGTCAACCCGGCACCAGCGGGTGCCGTTTACC GCGGGCTGCACAAATCCGACGGGTATGGGCTTGGAC  
CTGCCGACGGGGG

Clone Rv272

:::::::::::::Rv272SP6.seq:::::::::::::  
AGCTTGGCGTGACACCAACAGGGGCACTTAAGATGGCAATGCGCGGCTACCTGCAAGTTTTCGCGATGTCAGAGGA  
TGCCGAGGGGAGAACATCGGACCGCGCTGACGTTGCTCACCGCTTGGCGGGGTGACATTGGTGGTGGTTGC  
GGGCTGCGAGGCCGAGTCTAGGCCGGAAGCATATAGCGCGGCCGACCGCATTTGCTCTGACCGCAAGCGGACCTCA  
GCCGCGCGGTGGAGCTACTGCTGCGGCCATCACGCGCTAGGGTTCGGCGGGCTGCCGAAGCTCGGGTTGG  
CGAACTGCTACCGGGTCCGCGACGGCAACGAT

:::::::::::::Rv272T7.seq:::::::::::::  
TCATGCGCTTGAGCCGACCATCGAGTTAGTTGCCGAACCGGGGACCACCGAAGCACCGGCTCTGCTGCGGCACC  
GCGTGGCCCAACCGCTTGAGCACCACCAACCGCGAGCCCTCGCCCGCACGAATCCATCCGCGTTGGCGTCGAAGCTG  
TTGCTATCGCCGCTCGGTGACAGCGCCGACCACTTGGACAGCGCGATGGCGGTGAACCGGTGACAAGGTGAGCTGCACC  
CCGCCCCGCAATGCGAGCTCGTTTACGCGAGCGGAAGCTCTGACACGCCAAGTGAATTGCCACCAAGCAGCAGCAAC  
AAGCGGTATCTACGGCGATGG

Clone Rv273

:::::::::::::Rv273SP6.seq:::::::::::::  
GGGTGCAATTTCTGCAAGCGAGGCTACACCGTCTGCTGCTGGTATGCGATAGCCATCCCGTGGGCTACTGCCCAT  
CACCATCAGCTTCGCCCCGAAGCGCGCGTGGTGAATTTCCGCTGCGACCAAACTGAACGGGGCCAAACCGGTATTGCT  
TACCGCGCAACCGGGCCACCGCGATCGGCTCGGTTCAGGTTGGCAT

:::::::::::::Rv273T7.seq:::::::::::::  
AATCCGAATCTGACCGATACTTGAACCTGGTCTCGTTCCGCAATAACTCGTGGCGTGCAGGACGCGGCGCAACG  
TACTTCGGCATCAACCGCTCGACCTGAATTGGCAGCAAGCGCGCTGCTGGCCGCATGGTGAATCTTAACAGCAGC  
CTCTTCCCTACACCAACCCGACGCGCGCTGGCCGGGCGGAACGTGCTCTGCACCATGATCGAAAAACCTTC  
CCGGGAGGCGGATG

Clone Rv274

:::::::::::::Rv274SP6.seq:::::::::::::  
TTCCGAATTTGGGTTCNGGTGATATGACCTCATGGAAGAAGAGCGGCGCCCGCGCCGTCGACGCGCGAATGA  
AAACCTTCAACCGAGCGCATTTGAACGCGCAAGACGGTGAGCAGGTTCGAAGAGCTCTGGACGGTCTGGGTAAAG

09673476.113000

CCATGCGCCGAGCTGAACAGCTCGCTGTACAGCTGAACAGCACCGCTGGAGCGCTTGGAGGACGGTCTGGACCATCTCG  
AAGGTACCCCTGCACAGCTGGACGATCTCGCGAAACGGCTCATCGTTGGTGGCTGAGCCGGTGGAAAGCCATCGTCGATC  
GGATCGCATCATCGTAGCCTCGCGGAAACGGTGATGTACCGCTGTCGGTC

.....:Rv274T7.seq.:.....

NCTGCATCTTGGGGTACGTTCCGATGAGCGTGTGACCAACACCCGGCCAAAGCGGGTGGGACTGGATGGATACGGATT  
GCCATCATCGACCGCGTCCCGCTGCCGGTGCGGGCCAACCGGGAAGAACATCCGTTACTGTGATGACCAAGCGTGACA  
AATTGGGGCACGACTTGGCTGGGTGGACGATTTCACGAATCCGTGCATCTGCCCGGGAATTCGGCGGTGCTTGT  
GAAGGTGGCGCGGGGTGCCGATCTGCCGTGCGTGGATCGTCTGGTGTGGCGGTGGCGATTGTGCGCAGCAGCTGGC  
ACGGAAGATCTGCCAGCGCTGTGGACGGCGCCCGCAAGTGGCGCGCGGGTGTGGCTCGATGACCGACTGTGGTT  
CGGGTGTCCGCGCGATCGATAT

Clone Rv275

.....:Rv275SP6.seq.:.....

TCATCCCGACCAAAACCGGAGCTAGGTCGGCATCCGGGAAGCATCGGCACCGTGGCGCCGAGCGCGCTGCCGGCAG  
GCCATTAGCGGGGCAATTATTCGCCGCGCGCTCCCGGTCCGAGTACGGCGCCCCGAATGGCGTACCGCGCTGGTA  
ACCGCTCTGGCGGCGCTTGGCGCGCGCTCCCGGATCAGGTGTAGATGCCNACAAAGCCTCGTGATCGGTATCAC  
CAACGGTGACAGCAGCGGTTGTGCACCAAGCGCGAACGCCACCCGGTCTCGGGTCTGTCCAACCGATGACCGGCC  
CAAGCCCATATGAACAAACCCGGGCATCAGTTGCCGATCGGCATACCGTGA

.....:Rv275T7.seq.:.....

TTGGCGGGTTGGCCAGCAGCCCGCGGTGACGGCGACGATGCTGGGTGGTTGGCGCCCTGCGCCACCGCGGCTTGC  
ATGCTGGTTGGCTGTCTTGGGACGATCCGAAATAGTCCACGCGATCTGGTATTTGCGGGCTACCGCGATTACC  
CCGCGCGGTCCAGAGTTTTTGGCCTGGACTACCCGCGTGGCCAAATCTGCTGAACCTCGCGCGCGTGGTGGCCTGA  
ATGTCGAGCGCGCTTACTACGTGACCTGATGGATCGGGGGGTGGCGACCGTGCCCGGGGATGTGTATGTGCCGGGAN  
ACCGCGTCCGGTGGCCACGCAAAAGCCATGTCTTCGTGGTCCGACCATCGGTACCGGGACACGGCGCTGATTGGCT  
GGTTTCGTGCGAGATGTCGCGCAACTGCACGCGGCGGGCGAGCGGTGCTGTTANCCCGGAGGTTCCGGTGACG  
ATGATCGTGTGGTCTCCCT

Clone Rv276

.....:Rv276SP6.seq.:.....

GTAGGAGAGAAACAAAGACCGTCGATAGGACACGTGTTACGCGGTAGCTGTCTTGGTATGGGGTGGCGCTGCCGGG  
GGCATCTACTACCCGATCGGTTGTGGGAGGCGTTGCTGCGGGGCGACAATCTGGTCAACGAGATCCCCCGGACCCG  
TGGGACATCTACGAGTACTACGACCCGAAACCGCGCGTGCCCGGACGACCGACTGCAAAATGGGCGCGTACTCTGAT  
AACGTCGGGCACTTTGATCCCGAGTTCTTCGGGATCGGGGAGAAAGAACGATAGCGATCGATCCGACGACCCGCTT  
TTGCTGGAAACCTCTGGGAAGCCATGGAACACGGCGGGCTAACACCGAACCATATGCTTCCCGACANGGTTTTCGT  
GGGGTT

.....:Rv276T7.seq.:.....

CGAACTGAGCCATAGAAAGGCGAGCGACTAATTCGCTGGGCAATAGGAAGACCCCTTGTCTGCCAGTATATTTGT  
CCACTCGTTGCGAAGGAAGCGGCTGCGATTTGGTGCCTTTTCCCTGGGAAATCTCTGCCCGGAGCAGGAAGTCTTAT  
GAGTTGACAAAGCAGGGCGCGCCCTTCGCCGGAATCACATTCTGGTCTGTGAAATGAGAGCGCTCCGAGGTGGC  
GATGCTGCGAGCGCCGCGCCACGATACGACGCCATTCGCGCTTGGCGCGGTCTGCAACACCGCGGAGTTGTGGT  
CGTGGCATCTTATAGTGGCTCGCTCATCTCGCAGGCGACCCGCGATAGTGACGGGAGACCTGCGTCTGGTGGCGG  
TGAA

Clone Rv277

.....:Rv277SP6.seq.:.....

CTTAGACGCACTCCGGGCGAGCTCCACGGGTGGATAAGTACGGCGGATGTGGCGCAATGGGAAGTTGTTGCC  
CGCTTGACTGTCCGGGTTAACGCCGATTCCACACATCCCCTTGCAGAAAGCGCTTGGGTT

.....:Rv277T7.seq.:.....

GATCGCGATCGTCGATGTGGCATCCGCTTGGCGTCGACCCGCGTAAGGCAGACAGATGGTTCGGCGCACGCTCAA  
CTGCCACAGCACTGTAAGACTGCCCGCTCGCGGATTCGCGGTTGGTGAAGGCGGATGCTGCCGTTGCCGCG  
GGGCTGATGCTGTGGATCGACGATCTGATCGAGAGATCAGGCGGCTGGCTGGAATTGATGCCCGGATCGCGAT  
ACCGGATT

006274476-113000



## Clone Rv278

.....:Rv278SP6.seq.:.....  
AGCTTACGCGCGCTTTCGCTTCNGATTGGGACGCCGATCGAAAGCGCAGTTGGAAGCGCGCGCCCGGCTGGTCGAG  
CTGCTCAAGCAGCGCAATCCAGGCCATGCCGTTGAGGAGCAAGTGTTCGATCTTCTGGCAGCGCGGCTCAC  
CTGGACTCGGTGCCCTCGAAGATGTGCGCGGTGCGAAACCGAATTACTGGACCACATGCGGGG

## .....:Rv278T7.seq.:.....

CGACGCGGACCTCTGCGATCTTCCATAGCCCGCCACACCTTCAGTTGCTCACCAGGAATCCAACCGGTATAAGGTCGGC  
GAAGCGCTCGCGATTTGGTATCGGGATATGCGGCTCGGAGCGGTGAGATGCCCTCGGGTCCNGCCAGCACTTCCTCAGG  
CTTCGTGCGGGTGGTCGCGACCGGATGGGCCACATCGCATTCACAGGCTCGCGGATCACCAGACGTANACGGTT  
CTTTCTTAAGCAACACCGAAATTCAGGACCCGAATGCTCGGGAACATGTACAGGTAAGTCCGGTATTCGGGT  
ACCGGTTGAGCATTGA

## Clone Rv279

.....:Rv279SP6.seq.:.....  
CGGCATCGGTTTGGCGGTGCACGACAGTTGGTAGTTCTTCACTACTGTTGTTTCGAGCGTCGAGCGCCGCGCGGTGTC  
GAGGTGCGCGGACGCGTACCCGCGAGGCGGTCAGGGTGCCCTTCCAGTCCACGCGNGCTGTGGTCGGCTAACCGGTTA  
TCTTCAATCGAGACNATGCCAGCTTTCATCGTGTGGCGATCTTGTCCGAGGGCAGCTCGAACCGGCGCTGCGANTAC  
AGCCACGCGATCGTGTGGCTTCGCGTCGACCATCTGTCGATACCGCAGGCAATGCGCCCTCGAGCAGCTGGGCGGAT  
CGGTTGGCAAGCAGCTCAGAGGACAGATTGGACATCAGCCCTAGCCCGCGCTGCG

## .....:Rv279T7.seq.:.....

CCGTCGANGCGCGCACTTGGCTTGACGACACCAACATGGCTGAGGGTGTTCACAAAGACCGTGGCCGACGGGCTG  
AATCATCACCATGAGCGGCATGAGCCAGCGCCACCGAGTTTCATCATGTTGATCGCGGAAACCATTTGGCGGGTAGCGGAA  
GAACGGTCGAGGTGCTTACACCGAGTATTCGAAGTCGAAGGCGCAACCGCTGCTCAACGCGGCTCAACATCATTTTCG  
ACGGGTTTCTCGAGGAGGAGTGCACGATGAACGTGATCCAGGTGCTGTTGATCGCGTCGATCATCGGGTTGCTGTT  
CTACCTGTTGCGGTCGCGCGAAGCGCGGTCCTGCTGGGTCAAGGTGGGCTATGCTTTGTTCTGCTCCCGGCA  
TCTATGCGGTGCTGAGA

## Clone Rv27

.....:Rv27SP6.seq.:.....  
TTACACGNCCTGCTTCGGGCTCGTATGTTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGAC  
CATGATTACGCCAAGCTATTAGGTGACACTATAGAATACTCAAGCTTTTGAAGCGTCGCGCGGGGAGCTTCGCCGG  
CAATTTCTACTAGCGAGAAGTCTGGCCCGATNCGGATCTGACCGAAGTCGTCGGGTGCAGCCCACTCATTTGGCGAT  
GGCGCCGACNATGGCGCTGGACCGATCTTGTGCCGCTTGGCGACGNGAGCGGTTANGTGGTCAAGTCCGGTCTACN  
CTTGGGCTTTGCGGACGGTCCCGACGCTGTCGCGGTTGCGCCCGGGAAGCGCGGGTCGGGTGCCATCAGGAATG  
CCTCACCGCCGCGCACTGNACGCGCACTGCCGCGGCGATGTCNGCCATCGGGACATCATGCTCGGTTCTACTCTCT  
CGACC

## .....:Rv27T7.seq.:.....

CAGGCATCGAAGCTTTGTACACCAAGTGTTCGACAGGCGCTCCATCGGCGAGTGGATACTCCAGCAGGTAGCA  
GGTCGCCACCAACGCTGGTCAGTGCGGTTTCAGTCTGCTTGGCGGCTGCGACGCGAGTCCGGGAATAGCTGCCCTG  
CGCGACTTGGGATCGGACGTCGATGTTGCGGACGGGTGCGAAATCAGGTCGGCGGTAGCGGCTGCGGCTGATT  
GGACCGCTCATCGTGCCTTCGCGTAGCCGCGCCCGCACAGGCGCTCGGCTTACGCCCCCATCAAGGCGG

## Clone Rv280

.....:Rv280SP6.seq.:.....  
AGCTTAGCGAGTTTTTCTACTCTTGGGCGCACACCCACAGTGCTTCGACGGTAGCGGTACCCATGATGGCCATCCAGT  
TGGCATCGGTAGCTGATAAATCCAGCTGTTTCGCCAACCCGGTAGCGATCTTGGCGCGCTGCTTGTGTCACTGA  
TACCTATTCAGAGACAGCGCGGTTTGCAGCAAGATGACTTTTCGATCTCTTCGGGACATCTCGATGGGGTCTGTCG  
GAGTCCGCGGCGCACCGCGAGGTAGCCTCGTCGCCAGCCCATACCTCGACGCGAAGATCCAGGCTCGCGCAATAAGC  
CCACAGCTCTCTCGAGCGCGGCTGTAGCGGCTGGTTTCGACGGCAAGAAGTGGCCTCAGGCGATCTGTCGCGCGCG  
TCCCAACGCGCTGCGCGCGCACACCGTAGCGTAGCGCGGGCTC

## .....:Rv280T7.seq.:.....

CGCGCGGAATCAGACGCTGCTGGTGGTCGCGCATGCGACCGCGGCGACAAAGCGCACTTCTCGGGGACGACGAA  
CGACCGCTAGACAAGAGGGGCTGTCGCGAGGCAAGCGTTGTACACAGCTGCTGGCGTTCCGCGCCACCGATGT  
TTATGCGCGCGACGGGTGCGCTGCCACAGACGATGGAGCCACTCGCCGCGGAATGAAGTGAACCATACACACGA  
GCCCACCTTGACCAAGATGCTTACGCCAACCCCAAGCGGCGGACACCGAGTGTGAGATCTGTCGAGCAAGT

AGGCACACCCGTGATCTGCACGACGAGGCAAGTCATTCCCGATCTGATCACGTGGTGGTGCAGCGCACCCTGTGCC  
CCCGACAGTCCCGCAATCGCAAAGGCAGCACGTTGGTGT

## Clone Rv281

:::::::::::::Rv281SP6.seq:::::::::::::  
GTATTGTCAGCTGTCCATCCGGCGCTGTGGCCGAGCTGCCAGATCTCTGCACGCGTAACCGGGTTGCGGGATCCACG  
CTGTGGGGTTGTCTAC

:::::::::::::Rv281T7.seq:::::::::::::  
CCGACTTCCGCGGGTACCCGCTCAACTTTGTGTGNACCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCA  
ACTCATCTCTGAGCGCGGAACAATTTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCACGATGACCCAGTACT  
ACATCATTTCCGACGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCACTGGCGAAC  
TGGTTCAACCAACTTGAAGTGATTGTTAACTGGGCTACGCGACCCGGCCTATGGTTATTGCACCTCGCCGCCCAA  
TGTTCGCATCCGTTTCGGTTGTTCCAGAANGTCAGCCCG

## Clone Rv282

:::::::::::::Rv282SP6.seq:::::::::::::  
GCACCGATGTCGGCGAGCACTTCGTCAACTCCAGGGGTGCCCGCACCAAGTATTTTCGACGAGTATTTCCGTCGGGGC  
GCGCGCGCGGTGCGCGGCAGGTGGTCACTCTGCGCGCGGGCTGGGACTCGCGCGCTACCGGTGCCTCGGC

:::::::::::::Rv282T7.seq:::::::::::::  
TGACCCCACTTACTGAGCATGTAACGCTGGTCGTGCGGGTCTTGTTCCCGCTGTCGGCAGGGGCACACGCTCGGGG  
CGTAGCTGGGAGAGGCCCGGCTCAAGCCGGAGAGCAGTGTCTAGTCCGCCAGCTTGACCGACTTTCGATGAGAACGC  
GCTTTCGCGGTATTGAATCGGCGTCTGACGGTCTGTCAGCGTCTGAGCAGCGCTCGCCGAGTGCGGCCGCTGATTCTTTCATCG  
AGCCAGGACGCGCACTCTGTTCGGCCG

## Clone Rv283

:::::::::::::Rv283SP6.seq:::::::::::::  
AGCTTACGCGCGGTGACGCGACGAGTGGTTTCATGACACCAAAACCGTCAACGCTACTACAACCCGGGGATGAACG  
AATCGTCTTCCGCGAGCGATTTCAGCCACCATTTTCGATCCGAGGCCGACGAGGCCGCCAATACAGCGCGGGAT  
CGGGCGCGTGATCGGCACGATGATCGGCGACGGTTTCGACGATAGGGGCCAAATACGANGGCACGCAATCTGGT  
CNATTGGTGATCGA

:::::::::::::Rv283T7.seq:::::::::::::  
ATGTCGTCACTCACCACAATCGCGAGGACCAATCATGCCGCCAGGGCGGCCAACCAATGGTGCCCGGAAGCGG

CAGCTCGATCGACGCGGAGGTGCGCGCGCCAGTTGATTACGGAACAGGGTGAGGTTCATAGGCGGGCAGGATAGTG  
ACGAACGCAAGACCTATATCTGCGCTCGGAGTAAGAATCGAGTAGCCGGTGCACCAACGGAAGCGAAAGTGTCCGCGA  
TGTGTGATGAGCGTCGCGGTTGTGGCGGGGTGGC

## Clone Rv284

:::::::::::::Rv284SP6.seq:::::::::::::  
AGCTTACACAGCGTGCCGATGCTGTCGCNACACCTCCCTACTATGCGCAATTGCGCGACACGGGTGGCATCAACAGG  
GGCGATAAGGTGGACATCGCTGGGTTGAACGTGCGGCTGGTGCCTGCTGGCAATCCGCGGCAACCGGTGTTGATC  
GGATTCTCGTTGCCCGGCAAGCAATCGGGATGCAAAGCCGGGACGCAATTGCGACCGACACCAATTTGCGCGTAAG  
AACTGGAAATCGAACCCGCGGTTTCGGAGCCGTTGAAACCAACGGTTTCCTGCCGTGTCGCGCAAGACATACGCCA  
TACCAATCTATGACCGTTCGTC

:::::::::::::Rv284T7.seq:::::::::::::  
CTGCCCGGTGCGGTCAGCGCTGCGCAAGTCACCGACCGCGTCCGGTTTCATCGGACGGCTCCCCGAAAAGGGCC

CTGGCAACGAAAGTGCATCAATGAGCTCCCGCAGACCTTCGCCGATCTGGGACCGACATAGTGAAGTTTCGCCAGAT  
CATCGGCTCCAGCCCGGAGCAATTCGTTGAGTTCGCTGTTCGCGGGGAATTCGCGGCTGCTGACCGGGTCCGCCCG  
CAAAACCGACGAGGTGCACAACTCTTCGTCGAGGAACTCGGCGACGAGCGGGCCCGGCTGTTCCGCTCTCTTCGAGG  
AAGAACCGTTCGCGTCTGCGCTCCATCGCCCAAAGTGCACTACCGGACCTGCGACGAGCGGCAAGAAAGTGTGGTCAAGATC  
CACGGCGGGCATCCGCCCGCGGTTT

## Clone Rv285

:::::::::::::Rv285SP6.seq:::::::::::::

GATCTGCGCGGCCCGCCCGGCGGCAGTAGCAGATCAGCTCGTGCAGAAATCGCGGCAACCAGTCCAGTCGATTTCCATACG  
GGCGCGCTCAATCAACTCTGGGAACATCGCGATCGGCACCGGAAACCGCGGAGCGCGTCAGCCAGCGCAACACGAC  
CGGGATCGGATGAATCAATATATCAAGTGATTTCTGATGGCATCGAGCTCGGTGATCTTGGTCTCGGGGGCCCA  
GCTCGCGCTCGCGGACGTCGTGATCCGGCGGCCGAGCGCATAGACCGCAAATAGTGGCGCTCGCTTTTCGCGCGGCA  
AGAGTCGGATGCGCTAATATANGTTTCTGGCGGCCGTGCGGTGATCNACTCGGTGATTGATACGCTGTTTCATCTC  
GGTCATGCGCTCCTC

::::::::::::Rv285T7.seq::::::::::::  
GGTGGCGCAATGACCGAAACACCCAGCGCCCGCAAACCCGCGGCCCGCGCGGGCCCGCACATCTGTTCTGTTG  
GAGCGGCCCATCCAGACCGTTGGCGCGCGTAAGGAGGCCGTGTTACGAGTGCGGCTGGTGCCCGGACCGGCAAGTTC  
GACCTCAACGCGCGCAGCTTGGAGGACTACTTCCCAAACAGGTGCACAGCAGTGTATCAAGGACCCCTGGTCACC  
GTGGATCGGGTGAAAGTTTCGACATCTTGGCCACCTGGGCGCGCGGCCCGCTCGGTGTCATGGCGCGCGCGCTCGG  
CTGGGTATCGCCCGGCGCATGATTCTGATGTCGCGGATGACCGGCCCGCGCTGAATAANGCGGCTTCTTACCGCT  
GATCCACGCGCCCGCAACGCAAA

Clone Rv286

::::::::::::Rv286SP6.seq::::::::::::  
CACAAATAGATTACTCAAGCTTCGAACACAGCGGCTTATCACGTATCCCCGCTGAGACCTTGACCTTATGGGCGGAAGT  
GACTTCGCTGCTGCTATGCGGACACCCGATTTCCAGACGCTGCTGTACACGAGCGCGCGCGGTGGCCACCATCAC  
GCTCAACCGCCCGGAACAGCTCAACACCATCTGCTCCGCCCATGCCCAGCAGATCGAGGGCCGTATCGGTTGGCCCA  
GCGCGACCAAGCATCAAGCTCATCTGCTGCGCGGTGCCGCCGCGCTTCTCGCGCGGTACAACTTCGCGCGCGG  
GTTCCAACATTGGGGGAT

::::::::::::Rv286T7.seq::::::::::::  
TCAGGACGCTTATGTTGGCAGATGGTCGCCCTGGCGTCGAATACGCGCGAGCGCATGAGTCAACCGGTTCCGAACAA  
CGTATCGAAGAACGTCGCACTGCTGGCAGATGGTATCTCCGATGTTGTTGTAATTTGATCCCAACTCTAACTGTGCT  
ATCGGATCGAGCTGAATATCGAGATATTGCGAATGCGATGACAGGCCCGCATTCGGTTATTCGCTTACGCTTCCCGG  
GTTGATTCGCTGCTGACACTGCCGCAAAACGCGGATGATTGTTGAAACCGTATCTAACCGCAATTATTGATGTGGT  
AGCGCGCAGTGGCGCTTTGTGCTGTCGGGCTATTTCATCGGTTGGGGGTGTTGGCTATGCCCTCTGCTCCCAT

Clone Rv287

::::::::::::Rv287SP6.seq::::::::::::  
CGCAGCTGTGCGCGATCTGGTCGGAATACCTAGCTCCAGGTTCTGAGTGGAGATGAGTGGCGCATCGAAGTGTGT  
CAATGTACTCCAGGATGTCAGGTGCCAGGCCGCTGGCGAGGATCTTGGGCAACCGCGCCATGACTTGGTCGAAGTCGG  
CGAACGGGCGAGCAGCTGGCGTGTGTC

::::::::::::Rv287T7.seq::::::::::::  
GTAGTTCGTTCATCCAAACACAGTGGCGTACCGGCTCAAGCGGATCACCAGACTTACCGGGCGCGATCCCACCCAGCC  
ACGCGATGCTTATGTCTTCGGGTGGCGGCCACCGTGGGTCAACTCAACTATCCGACGCGCAGTGAAGCATCGACAG  
CAATGCCGTGTCATAGATTCCCTCGCGGTGAGAGGGGTCCAGCAGGGGCCCGCGAAAGATACAGGGGGCGCGCTC  
GGACCGA

Clone Rv288

::::::::::::Rv288SP6.seq::::::::::::  
TCCGCTCGCTTCCGAGAGGTTGAGTGCCAACGCTCTGCCGATGCCCGAAGCGGCGCCCGGTGATGACGCGCACCTT  
GCCTTCGATGAGCTCATTTGACTACTCCCCGTGGTTGCTTCCGATGGTGGAGGTGGCCGCGCAGCCTTGGCCCCG  
AGTTCGCGGATCGCTCTCGGGCTTCGGGGAGCAGACTGACCTGCAATGGGAAGTCTGCGACCATGCCCGCGAACCGG  
GATGTCTGATGCTTGTTTTCAAGCGGCGCAGGCGGTTTCGATCTTGTCCGCGTCAACACNGATCGGATGCTGCCCC  
GCGGTCTGATGACGAATGGGG

::::::::::::Rv288T7.seq::::::::::::  
ATGGGAGGCCACCGATACCATCTTGCACACACCGATTCCGGGCTATTGATGTCACGTTTCGGTCCGCGAACCGCGCT  
GTGGCTGTGCTGGCCAAAGGCGGAGGCGATACCGAAGTCAGTGCCCAAGCTTGGGTTCCACGCTCGCGAGCGCAGCG  
CGTCACTTTTCCACGAGACTCACTGCCGATCCGAAATGGAATCGGCCGTGACCGGAATTGGCGCAGCGAAGACTCAA  
CGAGGTGGTGGCTCTGTCGCGAACGTCACCCGAGTGGCGGTCAACGTCGCGCAGCGCGAGCTTCTACACCCGCAACCA  
GATCCGAAGCTGCAAGCTCCGACCCGATCCCGACGTCATCACCGTCCGCGCGGCGATCTTGAACCTATTTCG  
AGCTGGAATCGGCGCTCCGGTTGCTGGGAATTGCNGTTAAGAACTGGGCT

000217 54487-960

## Clone Rv289

.....:Rv289SP6.seq:.....  
GCTTTGCGCGCTTCTCCGAGAGTTGGAGTGCCAAAGCTCTGCCGATGCCCGAGCCGGCCCCGGTGATGACGGCGACC  
TTGCCTTCGAATGAGCTCATTTGACTACTCCCCGTGGTTGTCCTGCGATTGGTGGAGGTGGCCGCGCAGCCTTGCCC  
CAGGGTCCGGGATCGCGTCGCGGGCTTCGGGGAGCAAATGACCTCGAGATGGAAGTCGTGCCACATGCCCGGAACC  
GGCGATGCTCGATGCTTTGTTTGAAGCGGGCGAGCGGTTGCATCTTGCCGCGTCAACGCAGATCGGATCGTCGCC  
CGCGGTGTCGATGAAGAAT

## .....:Rv289T7.seq:.....

CTCACGAGCCAGCCGCTCACCTTTCACGAAGACCTCACCTGCCGATCCGAATGGAATCGGCCGTGACGGAAATTG  
GCGCAGCGAAACACTCAACGAGGTGGTGGCTTCGTGCGGAACCGTCACCCGAGTCGCGGTACCCGTGCGCACGGCGAC  
GTTCTACACCCGACCAACATCCGAAAGCTGCAAGCTCCGAGCAGCATCCCGAGCTATCACCGCTGCCCGCCGCA  
CGTTCTTGACCTATTGAGCTGGATCGGCCCTCGGGTTGCTGGGAGTGGCGTTAGAACTGGCCTAGAAACCGGGCGG  
GCACACCGCACCTGGGCGGGG

## Clone Rv28

.....:Rv28SP6.seq:.....  
TGTTCGGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG  
CCAAGCTATTAGGTGACACTATAGAATACTCAAGCTTGATGCCGCCGAAACGAGCGTGAGCACGCCGCCAGCCACC  
ACNCGCGGTCGGCGCCGGGCGCGGTGCGCANGCTGCTCGCTCGGTGATGGCAGCCACC CGCACACCAACCGCGG  
TGCGCTACGTCGAGCATACCGGGCGGAGCTACATCGGCTCGGCCGCCAGTGTTGGGGCCCTCTTTCAAGTCGAAG  
TCGATACCGATTGCGCATCCCGNCGCGCA

## .....:Rv28T7.seq:.....

CAGGCATGCAAGCTTCAAGTCCGTACGGTCGGGTACGCTTCGGTCGAGTGTGCGAGTGATAGATGACGACCGGGAC  
CTCGTCTGCATCTTCCATAGCCGCCACACCTTCAGTTGCTCACCGGAATCCAAACCGGTAGAAGGTGCGCGAGCGCTC  
GGCATTGTGTCATCGGATATGCCCTCGGGAGGTCAGAACCTCGGGTCGGCCAGCACTCCGACAGGCTTCGTCGGG  
GTGGTCGCGACGCGCATGGGCCACC

## Clone Rv290

.....:Rv290SP6.seq:.....  
GCTTGCTCATGTCGGCGCAGGTCGGGCCAGTCAAGGTGGAAGGCCAGTCCGGTCTCCTCTCCGACTACGGCCAAGA  
ACTGGGCGACGGTGTCAGTGCGAGACCAGCGGAACTGGTGGCGCCCTAGGGCAGCGACCGCCTCAAAACGGCGGTGA  
CCGCGTTCTGGTCGTGCACCATCGAGCCGTGCCAGCCCGCGCGTGCCGTCAAGCCGCATCCACTGGATGCCCTTCT  
CGCGGCTTCAATCAGGTACAGCGCAGCTTCGCCACCATCGTCCGGGGCACGGTTAGCGAGAAACCCCGACTTCA  
GATTGCTTCGTCGATGCGCTGGAACAGATCGGGCCT

## .....:Rv290T7.seq:.....

GCGCGCATGTTGAGGTTGTCCGACGGTGACGACGGTGAACCAACAAGTGTGACCTGTCCGCACACACCGTGTGGAT  
CGCGGAGCGGACCGACAAATCGATGGCGCGCACATCGCGTTGCCCGAGTGATTGCTAATCCGGTTCGGGGTCAAGTT  
GGGCCCCAATGACCCGGAAGTGGCGGTGAGTACGTCGAGCGGCTCGACCCGCAATAGCCGGGCGGCTGAC  
TTGGTGAGCAGGATGGGCAACCAAGGTCCGCGATCTGTTGCCACCATCGTGAGAGACGTCATGCGCCACGGGCAT  
CAGGTCATCTGGC

## Clone Rv291

.....:Rv291SP6.seq:.....  
TTGCGCTTCATGCCGAGCAAGTGCAGTCAGCGATGACGAATTGTTCTTCTCGCGGGTGTTGCTGCTGGTTCGGGCC  
TAGGAGACCTGCTCATATGATTAGCAATGTTTTCGACGCTGGCGACTATCCAGATCAGCTGACACTCCTTGCG  
CAGCAACCGACCTGATCCGCGCGGCATCGAGGA

## .....:Rv291T7.seq:.....

CGACGCTGGGCCCCAATCGCAGCCACAGGTCTGGTATGGCAGGACATGGCCGGGTTTCAGCGGCGCAATAACCG

## Clone Rv292

.....:Rv292SP6.seq:.....  
TAACGACTCGGGTCCAGCGACCGCGCCACACNAACGGCCGACNACGTGGGCGAGGTCGCGGCCCTCCCTACAAAC  
AGGATCCGTTGCCTGCGAACGACAGGCTCCGGTGGCGGCTGGCGCGCTGCTGTTCCACGCTCCGGTCCCGGGTGC

CCGGCGCAGCTTGTCTTCTCCATACTCGCCCCCTAATCTCGAGGCAGCCGTACCCGACGGCAACCTCCCAAAATGC  
AATCCCCAAAATGCAATGCTCNAGCTATTCTCACACCGACCGCTAGTTGCGGATCANAAATCCGTTGGCGCGGA

.....Rv292T7.seq:.....

CNTGGCGGTGGGTGCGGTGTCGAACACGACCACACTTCTTTGGCGGTTCGGTGATCTCGACACCGGCCGCGAGCCGACC  
ACCATGCGCGCATAGATCGCGCATCAGCGGTGCGGTATCGCTGGGTGCCGCCACCCGGAATCGGCCAGCGACCGGA  
ATGGGCGCAGCGTTGGCATCATCAGTCCGCGCGCGGCCGACACAGTAGCGGCAACCGGTGAAATCNGTGGGCGGCAAC  
GCCGTTGAACAACGCGCGGCATCTCGCCCGCCAGCGACGCCAGGCGAGGGGTGCCCTGGGCCAGCATCCGACGCC  
GAGACNAGGACCGANCCAGTG

Clone Rv293

.....Rv293SP6.seq:.....

GCTTTTCNGATCGCAGCGAGTCGTACCCGCGCCGTCACCTTCGTGGATATCGCCGCCCTGGTCAAGGGGCGTCCGA  
GGGAGCGCGGCTGGGTAAACAAGTTCTTGCTCATATCCGCGAATGCNACGCCATTGTCAAGTGGTGGCGGTGTTCTGT  
CAACAACNACTTGACTCATGTACCGGACGGGTCGATCCCCANTCCGACATTGAGGTCTGCANACCGAGCTGATCCCT  
GGCANATCTGCAACCTCGGAGCGGCCACGGGCCGGTGGAGAAGGAANCGCGACCAACAAAGCGCGCAAGCCGCT  
CTACAGCGCGGCACTGCTGCTGCCAGGTGCTCGACGCCGGAANACGCTGTTCCGCGCGGGGTGGATGCCG

.....Rv293T7.seq:.....

GTCTAGGCCATTNGTGGGTGTGCGCATACAGTAGCAGCGCGCGGGCACCTGACGCGCGCGCGCGACCACTGCGGT  
GCCATGCCCATCGTCTGCCACCCGGTCAACGGACGCACTTCTCTGGCCGACGTAAGTGGCGCCACCCGCGCGGTTG  
CGTCCCATCNATCCGGTCAACATGAGCAGCGCCAAACCCGAGCGGTACATGACATCGCTGTGGAACCAAGTGAACGTT  
CGCGCGCCCATGATGATCATCGACCGTCTCCGGATTGGGTGCGGTGCGGGCGAAATTCCTTGGCAACCGGATTGCG  
CTGCGCGCGCGCACACCGGTGATCGACTCTCGACGCGGGGTGTTCTGCTGGGTTCGGTCTGGTACCGGT

Clone Rv294

.....Rv294SP6.seq:.....

GCGAGGCGGTATCGTTCCCGTCTGACCGGCGACGCCAGCGGAGAAGCTCGTTTTCCAGTGTGCTGGGGATTCTC  
ACGCTGCTGCTGANTGCGTGCCANACCGCTTCCGCTTCGGTTACAACGAGCGCGGGGCTACGATGCTGCGACGCTG  
AANTTGGTGTCTCCATGGACTTGGGGATGTGCTGAACCGGTTACCTACNACTCCAAGCTGGCGCGCTCTCGTCCG  
CAGGTCTGTGCTTGCATAGCGGGAGGCCCGGATCCGCAATGACGGATTCCATGCCAACGCTCCGAGTTGCATCGCG  
ATCGAATACNAATTGATACCCA

.....Rv294T7.seq:.....

TGGGTCTTGCCGCGGAGCCAGCGAAGTCGCTAGCGTGCGCGTGTCTTCTGGCTTCGGATCTATCCTCGTTACATGAC  
CGGACCGGTGTTGACAGTGACTGGCGCGCGGTTCATATGACACCGAGATCATTGCCACGGTACGGCAATTCGTCAAGA  
AGGAAATCTTTCCNATGCACCGGCCCTCGAACGTGGCAACAGCTACCCGCAAGAAATCGTGGATCGGCTGGGTGTTA  
TTGGCTTGCTCGGTGCGCGGCTGCAAGGGTATCGACACCAACGAGTTCACTTCGCGCGCTGCCGCGCATTCGAGGTG  
GCGGTGCGCGCTGCCAGCAGCTCATAGTACTTGANGATGGTCAAACGTGCGGACGAACGCCACCAACGCTCGCTGCC  
GAACGG

Clone Rv295

.....Rv295SP6.seq:.....

TAGATGCCCAAGCTTGCCNTANAGACCTCGTCGACCAAGCAGGACGCGACCGTCAAGGTGGCGAATCCGGGCTTG  
CGGTACNACCGGCTAAGCAGACCATGGTTTCGCGGCAACGTCACCTGCCACGGCACTGGTAAGACTGCCCGCG  
TCGCGGTATTTCGCGGTGGTGAAGGCGGATGCTGCCGTTGCGCGGGGGCGGATGTTGTCGGGAGTGACGATCTGA  
TCGAGAGGATTACGGGCGCTGGCTGGA

.....Rv295T7.seq:.....

TCTCCAGCGGCTGGATCAAGGTACCGGCGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGCTTGATGCTCTGCGTTAG  
CGCGGATTCACACCATCTCCCTTCGCAAAAGTCGTTGGGTGCAATGATGACGCTCTCCCATCAGAGATGCG  
AGCAACGCAATCCGTGCGGTACGGTTCGGGCTGACTCGATGTCGCGACCTTGGCGTTGACACCATCTTTGTCATTG  
CGCGGAAAGTCGATCATCCGTAAGCGCGCTTATGACCGCCGCTTGTGCGCGGTTNGTAACTCCGCGC

000677-2425-1300

```

:::Rv296SP6.seq:::
ACGCGGTTCGATCGGGCAATCTCCGAGTCTGCTTACCGGAGGCGGTCTGGCGCGCTAATCGGCGTCGGCGCCGAC
GAGCTGTGGGATATCCGAATCGGGGCTCATCCCTGCGGGCGCGTCCCGCGGTCGAGCCTTGTGTCGACGCAATC
GAGGCAAGTCACGACGCGGATGAGGGGACAGCTGAATTACAGCGAGGTCGAGCTGTTGAGTCGCGCTCATCAACTGT
TCGCGGAAACAAGTCGCGGACCGGGTTGGAATCGGGGACACACACCTACCGGGGATCTGCTGTCCTGGGCTGCGGAC
CTCAATGTGNGTTCGGGCGCAGCCGGTCTACNACTCCGTGGAACACACCGGGGG

```

CTCGGCGTGGATATCTGGTGGAGCGGCGCGCGGTGAAGTGGGCTCTTACTGTCACTCGACAAAGCTCATAGGCGATC  
CAACCACTGANGAACCGCTCTCAGCAGTACCAACCGCGCGGCGAACACTGCGAGTTGAACCGGAGCTGCTTGGGTGATC  
TACTGCTCTCGCGGTTGTTCAGCGAGCGGCGCGAGCAAGGTAATGCGTCAACAGGCTCGCTAGAAAGCCGACAGCAAC  
GCGGCTCAACACAGCGATGTTCAGCAGCCGCGGTAGAACCGCGATGTGAAGACGAAAAAACCCAAATGTCAATAGCCGAATT  
CGGGGTGAGAGTGCACAAAGTCCCGCGTGTACACAACTGAACCTTCAACCA

```

1:.....:Rv29SP.seq.....:
TCCGGCTCGTATTGTGTGGAATTGTGACGGATAACAATTTCACACGGAACAGCTATGACCATGATTACGCCAA
GCTATTTAGGTGACATCTAGAAATCTCAAGCTTCAAGTCGTCGTCACGGCTCGGGTACGGTTCGGTCCGAGTGTGCGAGT
GATAGATAGACGACGCCGGAGCATCTCGTGGCAGATCTCCGATAGCCGCCACCACTTCAGTTGTCTACCGGAAATCAACCGGT
AGAAGTCGCGCAGCGCTCGCATCTGGTCATCGGAGATTCGCCGTCGGGACGGTTCAGAGCCCTCGGGTCGCGCAGCA
CTCCGACGGCTTCGTCCGGGTGCTCGCAGCAGCGCATGGCCACCATCGAATTCACACAGTGTCTCGCGGAATCACGACA
CGTAGAGGTTTCCTTCTTAAGCAACCAAGGAATTTCAGGACCGGAATGCTTCGGGAAATCATGTCA

```

CAGGCATGCAAGCTTGTATGTCGCCGAAACCGAGCGTGAGCACGCCGCCAGCCACCAGCCCCGGTTCGGGCGCCGGGGCC  
 CGGGCGGCCCGGACCTGTGTCCTCGGTGTATGGCACGCCACCGCGACACCAACCCGGCTCGCTACGTCAGGCATACCGG  
 CGGGAGCTCCAGTCCGCTCGGCCCGCACTGTTCGGGGCCCTC

.....:Rv25P6.seq:.....  
 CTTGATCCGGCTGATGTTGTGTGGAAATTGTGAGCGGATACCAATTTCACACAGGAAACAGCTATTGACCTGATTAT  
 CGCCAAGCTATTTAGTGTGACACTATAGAACTACTCAAGCTTCCAATCCCCTGCGCTGATACGCGTCGGCAACCGTGAA  
 CGGATATCTCGGCAAGCTCGGATCGGTTTTCATCCGGACAAAGCCGGCTGGCTACGGGTCGCTTCCTCGGCTAC  
 CACCCAGACGAAGTGTGCGAAGTGTGCACTTCGCAAGCATTTGTCATCAACCGCGAGCTGGGAACAACGACGCGATC  
 GAACCGTCGATACAGCGCTCNCNCGGAGAACTGGATGTTCGCTCGGTCACGCTCGGCTCGCTCGGTCACGGGCGAGCGGG  
 CGCTTAACATCAGTTGATCCCGTCGGCAAGCCGTCACCGGAATCGGGGAGACGA

CAAGATGATGCGCGGTGCCACCCGATCGTGCTCGGTGAGCGCGAAGTGTCTTCGCGTCCGGGACCAACATGTG  
GCAACGACCCGACACGAGCGCGACCGCGCGGCGCCGACATGCGCGTGATGGCGGACGACCGGACGCGGCATCGAC  
GATGGCGCGCAACGAGCGATTCATTTCGCGCGCGCGCGACGCGCATCGGCTACGAGTACACCAACACGCGCGGCG  
CTCGCTGAGGTTCCGCGCGCGGACGAGAACGTTCCGCGCGGTATGCCACGACGACACGCGCACCAGCGGGATCTGCTTC  
GGCCGCTGCTACGCCCTTGATGTAGTTGGCTGACCAAGCGGCTCGACAGCGCGTTCGGCTTTGTGCGGAGAGTTTCAGTGT  
CAGCGCTGCGACGAGGGGCGCGCGACGCGCGCGGCGCAGGTAGTGTACGCGGGGCTG

```

.....Rv301SP6.seq.....
CTCAAGCTTCGATCGACGATCATCCCGCTTCGGGTCTGGTCTCGAGCTGGTGGTTCATGGTCGGACCTGCTGGTAGT
GGGGATCTAAGCGCAACATGTCGGGATTCATCATGGTGTACCGGTGATACCATTCGACGCTGCCGGTGAACCCCGG
GATCGCGGATGATTCACCGCGCATAGGATGTCTGACCGCCGACCGCTCGCCGCGGATTCGGGATGTTCGGTATACG
ACCGCTCGGCAATTCGTCATCGCCGGATGCTCGAAGCTAGCCATGCCAACCAACCACTGTGACNACAATC

```

TGAATTTCCCGATCCACAAATCTCGGTTTCAGATACAGGTCGCCATACCCCTTACTTCGGCAACGCTGGGCGGATTGGC  
CCTGCCGCTGCAGCAGACCATCGACGCCATCGAATTGCCGGCAATCTCGTTAGCCAATCCATACCCATTCGACATTCC  
GCCGATCGACATCCCGGCTCCACTATCAACGGAATTTTCGATGTCGGAGGTCGTGCCGATCGATGTGTCCGTCGACAT  
TCCCG

## Clone Rv302

.....Rv302SP6.seq:.....  
TACTCAAGCTTGAACGCTGCGAGCGAGGCCATGTAGAGCGTTTGGTACCAAACCGATCGGTGGGCCAACTTGCCATGG  
GCTCAACAGCGGCTATCGCGAGCGTGTAGCCGATCATCGGCCAGGCGCAGGTGGCCTGAGCGGCGAGGGGTGCGCTTATC  
CATCTCTTGGCGCATGGTTGCCGAGGAGTGCCGGTAAAGTCTGGTGGCGAACCTGGCCGCTCGGGGTTGGGTTCTG  
GATTCCTCGGCTAGTAAGGTGCTCGCCTGGTGTACAAACGAATCGCTAGACAGCTCTTATCGGGAGTGGCCGTCGCG  
ATCGTTGCGCTGCGCGTGGCGATCGCGTTCGGCNTTACCGCCACCGGAACGTCCTCCAAAGTGCCTCATCGGGCTCTAC  
GGCGCGATCTTGGCGGATTTCTCCGCGGTGTTCCGTTG

## .....Rv302T7.seq:.....

GCGGTGTCGAACCTCGCCCGTTCCCTCCAGCGCATTGAGCTTCAGCCCGACCGGACGAGTGGGAGTCGGCATGCGGT  
CCTTCGCCCGGACCCCGCTGGCTAAATAGCCACCCCGAGCGCGGTACGGTCTTTGACCGGGACGACGGCATACCG  
GCAGCGCGAATCATCGCCGCGGCTGCAGCGTGAACGTCGAATACGAGTCGAACAGTGTGCGCGCGTAAAAACCGGAGC  
CGCGGTGCGCTTCGGTAATCAACGGCTCCTGCGCAACACGCTGCAANTCNCGGTGCCACCGGCGTTGACAACTTTGA  
TNTCGGCGACCTCGCGCACCAN

## Clone Rv303

.....Rv303SP6.seq:.....  
TACTCAGCTTCGGCTCAGGTGCTGCTGCTAAAGTTTNCCTGAACCGTGCAGGTTTCGACAAATGTTGGTGCCGGTTCG  
GCGGTTACTGCCATCGACAGACATGGCGCAGGCTATCGCACCCGTTTATCGGCTACAAACAAATCGCGGTATGCGTCTCT  
GAGCATGAGTCGGCGACGCTCGCTCATGGTCGACACCCACGACGGAAGACGAGATCGCGCTCAGCNGTGTGTGCGCG  
GGATTATACGAGTACGCTTCGCTGACACCGCNTGTTTGGTCNCGATGCTTGGCGCCCGCGCGGCT

## .....Rv303T7.seq:.....

CATCAGCTGTTTCATGAACTGGAAGCAGCGCAGCGCTTCTTTTCGGCCGCAACATGAGCCAGCCTCTCTGCGCGG  
TCGGGTGCGAGGTGCTCGGCGAGCTCGGCCGCGACAGCGCTGACCTGAAACACGCTTCATATCCGCGCAGCAAGC  
ACGCCAGTCCGCTACGTAACCCCTCCGCGACTGTCCATGAGCAACANCGCTTCTCCACCGACCGGCGCGGTTGTGG  
GGTGT

## Clone Rv304

.....Rv304SP6.seq:.....  
CTCAAGCTTCCCGCGCGCAGTACCGAAAGCGCAACAGCTCGCGGCGAGCCCAACNTGTGCGTGGGATGCGCGG  
GGCGANATCAATTCCAGCGAGCTCCCGGACAATGCGGCTCTGCTGGCCGCAACGAAGGACTCGAGGTACCCCGGCTG  
CCCGGGGCTGTTGTCACCTGCGCATCGCACAGGTTGGCCCAACAACCGGCGCTGATGCCCGGTGCGCAAGCCCGGCG  
AGTTGCCAAACCCAGCGTGATCAAGGCTCGGCTCGGAGTTCGCGGAAGAAGTGGCTCGCTGATCACCTACCATCGGC  
CAGGATCTGCGTGTATACNACGCTCGCCAAGGAGGTTGTTGTGGTGT

## .....Rv304T7.seq:.....

GCCAGCTTCGCGCGCGCCGCGTACCGCGCGGTACCGATCTCCGCGTCATACACCCCGGGTAATCGCCGACGGTGC  
CGGTTCCGAGCGGGAAGGTGAGACGCTGATTGAATCGAGTTCAGGTCCAGCGGGTGGCCGACCAACCGCGCGAGCT  
CAACGAGCTCAATCAGTTGTGCTTTCTACGGTCACGACCCGGTGACGCTAGTCGCCCGGTGCGCTCGGCCGAGAA  
GTTGACCGCCACACCGCGACACCGCTCTTGACACGGACGCGCACCCCGGATCGGTTGTTGGCCAAAGTAATTGGGT  
CATTCATTTGACGGGACCGCGACCCCGCAGCCCCAGTACCGCCACGACACCGCGGCTGACCCCACTCATGTACGA  
ACACCAAGCGCAGCGCGACCA

## Clone Rv306

.....Rv306SP6.seq:.....  
CTCAAGCTTGTGCGCGCTTAAACGAAGCGTGAGCAGCGCGCCACCCACACCGCGGGTGGGGCGCGGGCCGGGGC  
CGCGAGCTGCTCGGCTCGGCTGATGGCAGCCGACACCGCGCTCGGCTACGCTCAACGCAACCTCGGCGGA  
GCTACATCGGCTCGGCGCGCAGTGTTCGGGCCCTCTTTCGAGGTCNAGGTCNATACCGATTTCGCGATCCGACGCG  
CAACCTGGACACAGAACCGTGCCCTACGAGTGCTTGTGCGGCGGGGCCAAAGAACANCTTGGCATCTTGGCGGAT  
GGCGGCGCGGCTCTGGTC

## .....Rv306T7.seq:.....

CTCGGGTACGCTTCGGTCCGAGTGTGGAGTGATAGATGACGACCGGACCTCGTCGGCATCTTCCATAGCCCGCCAC  
ACCTTCAGTTGCTCACGGGAATCAACCGGTANAANGTCGCGAGCGCTCGGATTTGGTCATCGGGATATGCGGCTCG  
GGAGGTCAGAGCCCTCGGTCGGGCGGACGATCCGCGAGGCTTCGTGGGGTGGTCGCGACNCGCATGGGCGACCATC  
GCATTCACGAGTGTGCGG

CAACAGCGTTCCAGCGGCATACCACGCGCATGCCGTGCACCCGGCGCCGGGCGGAGTCGCCGCATAACACANGTACA  
CCTTGGAATCGTTGCGCGCAGGGATTCNACCGCGGGTGGGGCGGCGCATGCCGCGCAGGTGAGTTGCGCCGCA  
CGTGATNTACCCGCGCGTAGTTGCGCTGTGGTCCGCCATCCGCGCGGCGCACGGCGCGGCCGCCACCCAGA  
TGGTCAAGCAAGCGGGGCGGAACGCTCGACGACTGGTTACGCTCNGTCGNCNTNANCGTGAACCGACNGACGT



GGGCATATGTCCANAACGGACGNGGCCGGTTTCNTCGATGCNGCCGGGTCGCGACNTGCGGACNCCNGNCACACC  
ATCCGCCAGTCCGCGTGGCGTCCGCCCGGACTCTGCCTCGGCCGCGCCA

## Clone Rv310

.....Rv310SP6.seq.....  
CTCAAGCTTTTNGCAGCATCGGGCGATGTCGATGANAGGAAACCCAGCGCACACCGGACNATTTTGGCGTAGCCGGC  
GGACNTCTGCTCGATTCCGATCAGCTCGGCGCTCGCATCGAGCATGGCGCCGCGACGGCTAGCAGCGATCCGCGCTC  
GTCCAGGAACACGACAGCCGATCGCCCGCGCTAAGCCGCGCCAGGATTCGGCGAAAAACCGTTCTACGTGGCG  
GGTGTACTGGGTGTCCAATGATTCTGCGGGTGCCTAGCGCTCGCTGCAATCGTCGACATAAATGCCCTCGGCCCGCAT  
CGCGTCACAACTCCCGGGTGAGTGAATANCACTTGCCGA

## .....Rv310T7.seq.....

TCCAACGCGGTGACAGATTGTCTATCTGGACCTGACGGTGAGGTGGAAGTTTCCAGGAATTCCGCAAAATCGGTA  
AGAGCCTGAAGAATTCCGATATCGCCGCGAGAAATCTGCGACGCATACGGGGCAGATACGCTTCGGGTTTACGAGATGT  
CGATGGGCGCGCTGGAGGCTTCACGTCCATGGGCCACAAAGGATGTTGTCGGCGGTACCGTTTTCGCGACGGGTGT  
GGCGCTTGGTCTCGACGAGCACACCGCGAAACTCGGGTGCTGACGGCGTGGAACTCGACATCGATACGCTACGGG  
CGTTGACCGCACCATCGTCGGCGTGTC

## Clone Rv311

.....Rv311SP6.seq.....  
CTCGTCTTGACTACGCCAGTATGAAANCTCCTGTGCGGGTNCGTAAACACCCGGCGGACACTCANACGGTGCT  
GGTGGTGGCGCATGGCACC CGCGGCGAGCAAGCGCATCTCCGGGGACGACAGCAAGCGACCGCTAGACAAGAGGGG  
TCGTGCGGCGAGAAAGCGTTGGTACCACAGCTGCTGGCGTTCCGGCGCACCGGATGTTTATGCCGCGACCGGGTGCG  
CTGCCACCANACNATGGAGCACTCGCCCGGGAAGTGAACGTGACCATACACAGAGCCNCCCTGACCGAAGAGTCT  
CTACGCAACACCCCAACCGCGCGGACGACGAGTGTCTGAGATCTTCG

## .....Rv311T7.seq.....

GTATGCGCTCCNCTTTGGGCCACGAGCACCACAGCGCGGTTTCGGGACCGGAACGTGGACATCAATAGCCCGGAATCG  
GTGTGTGCAAGTTGGTAAACGGTGTGATCCAAAGCTTTGCCAGGCTTTTCGTAGTCTTGGGCGCCACACCCACAGT  
GCTTCGACGGTACGGTCACCATGATGGCCATCCAGTTGGCATCGGTGAGCTGATAGATGCCAGCTGGTTTCGCCAAC  
CCGGTAGCGATCTTGGCGCGCTGCTTGTGTCACTGATACCTATCGAGCAAGACAGCCCGGTTTTCGCAAGATGACT  
TTTCGGATCTCTTCNGCGAACTTCCAATGGGGGTCTCCGGGANT

## Clone Rv312

.....Rv312SP6.seq.....  
CTCAAGCTTTTGGTCTAGCGCGCGGACGACGATACGGGTGTCTTGGCCACCGCGCGGCTGTCCGGGAATGGCGG  
GTCCCCGGTGGTTTTGCTGANGANTGCTGAACCGTAGTCGAAGTGGGCGCGCTCAGACTCCACCCAGCCAGCGGAC  
CGCGAAGCTGAATCCTCAACCCGGGTGTCGATCCGGACAGGTTGGGGTGCCTTTGGGGCAATGACAGGTGGCGGGG  
TGGCTTGGGTTCGGGTCCGGCGCGAGGTGCTGCGTTGGGATCNCCTGGGTGGGCTTCGGCNTNTTGGCGCGCGCGGTTG  
TGGGGGGGCAACANGTGTCCGGTGGGGTGGCGCTGC

## .....Rv312T7.seq.....

ATCTGTACCGGACCAAGATCTACACCATCGAATACGACGGCTCGCGGACTTTCGGCGGTACCCGCTCAACTTTGTGT  
CGACCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAACCTACTCATCTGACGCGCGGAACAAATTGACGCGAG  
CGGTTCCGCTCCGAACATACGGTTCGCTCCACGATGACCCAGTACTACATCATTCGCGGAGAACCTGCCGCTGCTAG  
AGCCACTGCGATCGGTGCCGATCGTGGGGAACCACTGGCGAACCTGGTTCAACCAAACCTTGAAGGTGATTGTTAAAC  
TGGGCTACGGCGACCGGCTATGTTATTTCGACCTCGCCGCC

## Clone Rv313

.....Rv313SP6.seq.....  
CTCAAGCTTTCGAATCGGGGTGCGGATGCCCATGGTTGGGAATGGTTCGCCCTGGCGTCAATACGCGCGAGCGCATGA  
GCTACCCGGTTCGGAACAACGATCGAATAACGTCGCACTGCTGGCAGATGGTATCTCCGATGTGGTTGTAATTTGTA  
TCCCAACTCTAAGTGTCTATCGGATCAGCGTGAATATCGANATATTGCGAATGCGATGACAGGCGCGCATTCGGTTT  
ATTCGCTTACGCTTCGGGGTTCGATTCTGCTGATGCACTGCCGCAAGCGCGGATATGATTGTTGAAACCGTATCTA  
ACGCAATTATTGATGTGGTAGCGCGAGCTGCCGTTTTGTGTGTCG

.....Rv313T7.seq.:.....  
CAATACACGCCGACGACAGCGCGGACATCGCCATCCCGAGCAGACCCAAACAGGGATACAGGATGGAGCCAAACGC  
CAGGCCCGGCCAGGATACCAACCAACACCGGCTTGGTCAGCTTGTCGGCGCGGTATAGGCATCGGGCCGCTGCAA  
CGCGCATGCACAAACGCGTACACCGCTGTCAACAGACGGCGACCAAGCAATACAGCATGACGGTACCCACGAGGTG  
GCTCAGCATTGAGCATATGCGGTTTGATCCAAACAG

## Clone Rv314

.....Rv314SP6.seq.:.....  
CTCGTCTTCGGCCTCGCTGCAGGAGTGGGAGCCGACGGGCTGGAATCCGAAAAACAGCGCGGTGATCGCACTGTCG  
CCGATCGGCGCCGACCTGGTTGGTGTACGGATGAATCCGACGCGAAATGTGGCTCGGTTGGCTGTCTGACTCGT  
TGGCTGCACGCTGGTGGCAGCACCGAGCGGTTGGTCCAGGATCTGGATGGGCAAAAGTTGTGCGGCCCGCGCGGTGA  
CGGCCGATGAGTGAACGAGTGCAGACGCGGCTGTTGGCTGACTTGAACCGACATGAGATCGCCCCGGTT

.....Rv314T7.seq.:.....  
GTCTAGNCCGCGAACAGCATACGGGTGTCAATTGGCCACCGCGCGGCTGTCCGGGAAATGGCGGGTCCCGGTTGGT  
TTTGTGAAGATGCTGAACGCTAGTCAAGTGGGCGCGCTCAGACTCCACCCAGCCAGCAGGCGACGCGAAGCTGAA  
TCCTCAACCGGGTTGTCGATCCGGACAGGTTGGGTGCGTTTGGGCAATGACAGCTGGCGCGGCTGCGTTCGGGTC  
GGCGCGGGAAGTGTGCTTGGGATCGCCCGCTGGGCATTGCGCGTGTGGCGCGCGCGGTGG

## Clone Rv315

.....Rv315SP6.seq.:.....  
ACTCAAGCTTGAGATTGGCGTCAACGGGTGTGCGCACCGCGCGTCTCGAGTTGGTAGGCTCGAGTTTGTGCATCAGG  
CCGATGCCCGCGCCCTCGTGGCCACGCATGTACANACCAACGCCCGCCCTCAGCGGCGACCATCGCCAGCGCGGCG  
TCCAGCTGAGCGCCGCAATCGCAGCGCGTGAACCAACACATCGCCGCTCAAGCACTCCGAATGCACCCGAGACAGC  
ACGTCG  
TCACCGTGGCGGTTGGGCGCGCATCTCGCCGCGGACAGCGCGACATGTTCCACGTCTCGTAAATGCTGGTGTAN  
CCGATGGCGGCAAACTCCCCATGCAANTCGGAATCCGCGCCTCGGCGACCCCGCTCAATGTTGCTTCTCNTGCTTG

.....Rv315T7.seq.:.....  
TCGACNAGCATCTTGACNGTTGTTTGGCTCGGCATGGTTAGCCAAAGTTCTCGGCTCCCACAGATCACTTTGGTC  
CGGTAGCGCTCTGTCGGGTATGCTGCCCGGGATTCTCGCTGGTATTACTCCCCCGAAGACGCGACCGGCTCGAGC  
GGTGGGCGCGCGGTTCCCATCAAACTGAACCCCAACAGGGGACATGCTTAGCGGTAGGGCGCGCGCAAGGC  
GGACGAAATCGCATCACTGCGCTGCGCGTCACTATTAAACCAACCGGACTTCACTTCCAGACCCCGAATGGCGCGG  
GTCAATTGATCATCTTGCGCACCGCGGATAATCGGGAT  
TG

## Clone Rv316

.....Rv316SP6.seq.:.....  
ACCGGGGCACTCGGCACAATCTGTACCGACCAANATCTACACCATCGAATACGACGGCGTCCCGGACTTTCCGCGG  
TACCGCTCAACTTTGTGTNACCTCAACGCCATTGCCGCGCACTACTACGTGCATCCAACTACTTCACTCTGAGC  
CCGGAACAAATTGACGCGCGGTTCCGCTGACCAATACGTCGCTCCCACTGACCCANTACTACATCATTCGACG  
GANAACCTCGCGCTGCTAAAGCACTGCGATCGGTGCCGATCGTGGGGAACCACTGGCGAATCTGTTCAACCAAC  
TTGAAGTNATTGTTNACCTGGGCTACGGCGANCGGCTNTGGTTATTCCACTTCNCCGCGCAATGTTTGNACTCC  
CGTTGGGGTGTGCCNNAAGTCAACCC

.....Rv316T7.seq.:.....  
CGCTCAAGCGCNTGAGGCCAANCGGCTGGTTACGACTCCCTGTTTGTGATGGACACTTCTACCAACTGCCCATGTT  
GGGAGCCCGGACGAGCGGATGCTGGAGGCTACACGGCCCTTGGTGGCTGGCCAGCGGACGAGCGCTGCAAT  
GGGCGGCTTGGTGACCGCAATACCTGCAGCGCCGACCTGCTGGCAAGATCACTACCAGCTCGAGCTGGTTAG  
CGCGGCTCGAGCATCTCGGCATTGGAGCGGTTGGTTGANTGGAACACCGCAGCTCGGCTTCGAGTTGCGCAC  
TTTCAGTGACCGGTTCT

## Clone Rv317

.....Rv317SP6.seq.:.....  
CTCAAGCTTGCCTCGATGAAGTAGTCTGCGGTGAGCGCGCCCTCTTCGAGCTCCTTGGCGATGCCAGCAAGGATC  
ATCGCGCGCGAGCTTGGCCAGGATCTTTCGGCTCTTCTTACGATGCGGGGCGCGGATCGTAGTCTTGTAGAC  
ACGATGACGCAAACTCAATTGTACCCCGGCTCGCGGTTCTTGACTTTCGCTACAAACTCGCTGACGCTCGTGGC

GCTGTCGCGAATGCCCTCGAGCATCTCCAGGACAGCCTGATTGGCGCCGCCATGAAGCGGACCCCATAGTGCCTGTATGCC

::::::::::Rv317T7.seq::::::::::

GGTCAGGCCGAGCAGGCGCGAGGAACGACGAACCAACAGCCATGGTGGTTGGCGCCGTCGAGAGGTGCGGCGTCCG  
CACAAACGGGAAGATCGCCTTGAGCGTGCCTCGACCGCCGCTCGAGTTGGGTATAACGAAGTAGCTGATGCCGATCA  
TGTGACGCTTTTCGTCGCATCAGCGTGCAGCGGCGACCCACTCNACGAGGTCTCGGTGCCGCCGCGCCAGGGCACC  
GCGTGCAGAGTCCAGCGCCGTCGCGGCAAGCAGTGCCTGCTGCCANCCGTGGTGGGTGCGGCGATGTTGGGTGTGC  
TCATTTTCGGGAACGCCA

Clone Rv318

::::::::::Rv318SP6.seq::::::::::

CTCGAAGCTTTAACAGCATCAACCCGCGCCGACACGACACNATGTGCATGCCATCGAGGTGAATGTGCAAC  
TGGCGCAAAACCATCGGCGACCGCGACCAACCGCAACATGGGTACCGGCGATTTCCGGTGCCCAATGCCGACCCGACGGG  
CCGCTCTCACCGCAGGTGACCTTCGATCACCAGACCANCCGCGCTTNTNNTCAGCACCCCTACCGTGTCAAGCCCA  
AAACGCGCTGGTGGTGCATTTGCCGAGTGACCCCNACCCAGTGTGTCGCCCGGATCC

::::::::::Rv318T7.seq::::::::::

TGATGCCGCGCCGATCGACGCTGTTGGTTCGGGTTGACTGGCGCCCGCGCAAGCAGGGCGTCGACCGCGGCCGCGG  
ACGTGCGCGCGCGCTCACCGCTCGGCCATTTGCCCGCGCGGAGTCGTGAGCTGACCAGCGTAGACAAGTCGCGCGTGG  
CCGTCGAAGACNAACGTGTGCGGTTGTGACGGCCGCGGAGAAGCGCGGCGACNTCTTGGGTTTCGTGCTANAGATAC  
GGGAACGTCCAGCGGTGCGCGCGGCCCTCGCGCAACATCTGATCGGCGCGCTC

Clone Rv319

::::::::::Rv319SP6.seq::::::::::

TTTCGGGCGAGCGGATATANTCTCCNTCTGACCGGCGACCGCCAGCCGANAAGCTCGTTTCCCAGTGTGCTGGGG  
ATTTCAAGCTGCTGCTGANTGCTGTCGCAAAACCGCTTCGCGTTTCGGGTTACAACGAGCGCGGGGCTACNATCGTGGC  
ACGCTGAAGTTGGTGTCTCCATGGACTTGGGATGTGCTGAACCGGTTTCACTACNACTCCAAGCTGGCGCGCTCT  
CGTCCGAGGTCGTTGCTTGCAGTAGCCGGGAGGCCGATCCGCAATGACGGATTCTNCCANCGCTCCGAGTTGC  
NTGCGGATCGACTACNATTTGATCACCANAACCATCGGCGNTNTACTGCCTGAAGTACCTGGTGGGGTCGGATAC  
TGCTATCCGCGGTTGCAACCCCGCAAGC

::::::::::Rv319T7.seq::::::::::

GTTTTGGCTCGGCATGGTTAGCCAAAGGTTCTGCGGTCCACACAGATCATCTTGGTCCGCTAGCGCTCGTCCGGGTATG  
CTCGCCCGCGGATTTCTCGCTGCTATTACTCCCCCGAAGAACGCCACCGGTCAGCGCGGTGGCCGCGCGCGTCCCCA  
TCACAAACTGAACCCCCAACAGGGACATGCTTAGCGGTAGGGCGCGCGCAAGGCGGCAAGCAATCGCATCACTGGCT  
GCGGTCACATATTAAACCCACCGGACTTCACTTCCAGACCCCGAATGGCGCCGCTCAITGATCATCTTGGCGACCG  
CGGATAATCCGGGATTGCGACGCCATTCTNACTACCGCATGCGAGTCTCGGCTGACCCGAGGCTC

Clone Rv31

::::::::::Rv31SP6.seq::::::::::

TCGCTAGCGCGGCTTCCCCTTCCGTCCGAGCNGTCAGAAGCTCCTATGACAAATGCACTACCCGAGACNATCAACGGC  
CTATGCAATACNAGCTGATCAAAACCGCAAGCCCTGGCGGTCCATCGAGGATGTCGAGTTGGCCACCGCGCGCTGG  
GTCGACTGGTTCAACCATCGCGCCTTACCGGTACTCGCGGACATCCGCGCGGTCTAATCGACGCCGCTCACTA  
CGCTCAACGCCAGAGAACCNACCGCGCTGACGTCTCAGATCAGAGATCTCCGGACTACCGGGGCGGTTATCCCC  
ACTGTCGATAGCGTCTGTGGATAACTTTGTCTGCA

::::::::::Rv31T7.seq::::::::::

GCGCGTNGAAGTATAGGTGCGGCCGCGCTCGAGCANCGCGGCATTGTTGTCATGCGGTACCGAAGATCTCTTCGG  
TGACCTGCCCGCCGCGGCTGCTCGGCCAGTCCCGCGGTTGGCGCCGCGCGGACAACTCTTGGCGTCCACGGTGG  
TCTGGGTCA

Clone Rv321

::::::::::Rv321SP6.seq::::::::::

CTCAAGCTTCAATACAGATTATAAACTGTGATAATCAACCTCATCAATGATGACNAACTAACCCCGATATCAGGT  
CACATGACGAAGGGAAGAGAAGGAATCAACTGTGACAACTGCCCTCAAATTTGGCTTCTTAAAAATTACAGTTTC  
AAAAAGTATGAGAAATCCATGCAGGCTGAAGGAACAGCAATAACTGTGACAAATTACCCTCAGTAGGTGAGAACAA

000571 94242960

ATGTGACGAACCCCTCAAATCTGTGACAGATAACCCCTCAGACTATCCTGTCGTCATGGAAGTGATATCGCGGAAGG  
AAAAAT

## Clone Rv322

:::::::::::::Rv322SP6.seq:::::::::::::  
CTCAAGCTTCGATCGACATTACTCCGCGCTTGGGTCTGGTCTCCGAGCTGGTCGGTCATGTCGGACCTGCTGGTAGT  
GGGGATCTAACGCAACATGTCGGGATTATCATGTGGTACCCGTGATACCCATTCCGAGCTGCCGTTGAAACCCCGC  
GATGCCGGGATTTCCAGCCGACATAGGATGTCTAGCCGGCCAGCCGCTGCCGCCGGACTTCGGGATGTTTCGGTATACC  
ANCGATCGGCAATCTTGGCTATCCGCCGATGCTCGAACGCTANCCACGCCAACCAACCATTGTGACNACAATCGCCA  
CCACACCAAGGTCATGCCCTCGGCGTATGTCCGGTGCCGAAAGCCGCCAAGAGTCCGACGCCGCC

## :::::::::::::Rv322T7.seq:::::::::::::

CATTCCCAATTGAATTTCCNATCCCAATCTCGGTTAGATACAGTGCGCCATACCCCTTACTTCGGCAACGCTGG  
GCGGATTCGCCCTGCCGCTGACGACANACCATCGAGCCCATCGAATTGCCGGCAATCTCGTTACGCCAATCCATACCCA  
TCGACATTCGCGCGATCGACATCCCGGCTCCACTATCAACGGAATTCGATGTCGGAGGTCGTGCCGATCGATGTGT  
CCGTCGACATTCGGCGGTCACCATCGAGCCACAGGATCGACCCGATTCGGCTGAATTCGACGTTCTCAGCAGCG  
CCGGACCCATCAACATCTCGATCATCGACATTCGGCGCTGCCGGGCTTGGCAACTCGACCAGGTCGCCGCTGTCGG  
GCTTCTCAACACCGCGCGGTGGCGGT

## Clone Rv327

:::::::::::::Rv327SP6.seq:::::::::::::  
CTCAAGCTTTCGGCGAGACGGACANNTTGCGAACATTGATGACAAAATAGAAATCATTGATGGTTGAGTCACAGG  
CCGATCAAGCTTCGCGGAGGCCAAATCCAATCAAGAGGCCCAAGCCGTAACCAATCAGCCCGGCAACGAGGGATTCC  
GTGATATCAGCCAAATAATGCTCTCGGGTTACACCCAAACAGCGCAATATGGCGAAAAACGGTCGCCGTTGCACG  
ACATTAATGTTCACGGTATTG

## :::::::::::::Rv327T7.seq:::::::::::::

AGCTTAACGTGCTCCCTAATACCTGGGGCTGTGCTTCGGGTGATGCAGGGCATACGGACATCCNTCCCTGAGACCCN  
CGGTTCAATCAGCCAGCTGTCCACCATCAGGGGTTCAACCCGGGCAAGGGCAGCGCAACCAAGTTTCGCGACCGGTT  
AACCATTGTGCTGTGAGCTTCATTGTGCTGCGAGCAAAACAGTTGGTCGGCCGTTAGGAATCGAATTGACACTCAACCGA  
TTTGGTGCCNCCGTAGGTGTCTCGGCTGCGGGTGCGCTGGTGTTCGCCGCTGGTAACGACCAATGTGACCGGG  
GGAGGTGAACCACTGGCCACGCGTCCGCGAATGTCTATTGCGGGG

## Clone Rv328

:::::::::::::Rv328SP6.seq:::::::::::::  
CTCAAGCTTGGGGTGGCGCTGTCGGTGGTGCTTGGCGGCGTCGGTATCAACACCGCCCAAGAAATGGGGACAAG  
AAGGATTTCGTTGAGCGGTTGGCTGTCCAAAATACCCCTCGCCCCAGCTGCTACGGGCACTTCTACATCGAGCAACA  
CGTGCCCATCACGTCCGGGTGTCACACCGGAGGACCCGGCGTCGGCGCGGTTTCGGCGAAACGTTTGGGAGTTCTGT  
CCCCGACGTGTTATCGCGGCTTCGCTCGGCCCTTCATTGGAGGCCCAACGGCTGCTGGGCTCGGCTCAGCCCC  
CT

## :::::::::::::Rv328T7.seq:::::::::::::

GCACCAAGGCCCAACAGTCACCTGTGACCTCCTGCGCGGACCCCGCCGAGGTCCTGGCCGTTACCACTGAACGG  
GCGAGCCGGGAGTCTGTTACGATCGCAACAAAGCAAGTGATGGGCGGAGTTGTTCCGCCACTTCGTGATGACG  
GGGTCTATCCATTTCGAGGTCGCTCGCGCGCTCGGTGCAAGTGGCGGTCACACTCCAGGTACTCGACCTCACAGACGAG  
GGACTCGATCCCATCTAGGTGTGACGAAACAGATCTTCTGTCCGA

## Clone Rv329

:::::::::::::Rv329SP6.seq:::::::::::::  
TCGCTTCGCGATATGGGTGCGAGCCAAAGCGGGTCGGGATTTCTGGGCTTCATCGCTCGCGCCGTCGCGACAACACAGG  
CGGCTCGAACCGACACTCGTTGTGATGTCAGCTATCACTTCGGTACGACCAATCGACCCCTACNCGGCTATCTCA  
GCGCGATCTCCAGGCTCCGCGAGCCAGGTGCATCCCGGTCCGGATCCCACTAACCCGGCACCATTTGGCGTCN

## :::::::::::::Rv329T7.seq:::::::::::::

GCTCTCGAGTGCCCGCTCGNACNCCAGCGCCGCGCGGCCACTTGGATGCGACCCGTTCAAGTCCCTTCATCAT  
CTCGGAAAGGCTTGAACCATGGCTCGGCCAGGATCGCGAGACCGGACCCGGAGGTTTCGAACGACAGCTCGCA  
GGATTCGACGCCCTTTGAACCCACTTCGGCAAGTCCCGGACACCGTGATTCGCGCCCGGGTTCGACGACACGAT  
CGACATCGCTTGGTGCCGCGGTGTGGCGTTCGGGTTCG

## Clone Rv32

.....:Rv32SP6.seq:.....  
GGCATACCAATGTGGGACTTCTGCTCAACCACGATATCCGTGGTCTGATCCGCTGCTGCGGGGGCTGCNACCTGCNTC  
TONGCGGCACCCGCTNACTACATGGCNCGCCGACGCATACGTGCGCGCGGGACCCACTCCNACTGGTGCAGCGGTGC  
TGCGCGCGTCTGCCGANTGCCNAAACCGGCCGACCGACGAAACCGGCCGCCGTCCGTCTTGAGCAACCGTCAATGT  
GCCGTGCGGGTCTGATGCTCGAGCCCATCGAGACCGTAACCAAGCGTCTCTGAGCGGGTTCGGCTTCGGCTTCGGTGA  
CTTCGTGGCTGCTCGCGCGCTGCGGCCGCGCGGATGGTCGACCAACAGCCCAACCACTCGCGGGTGACATACCGTCT  
CGGCCACTCGACTGGCGCGGATGCGGGCCC

.....:Rv32T7.seq:.....  
GTGAGCAGACCTACGCCNCTGGTTCGCCCAACTCGGTACCGATCATGGCGCGNCGCTGCTGTCACCGATACCCAGC  
GAACAAGACAGCCCGGTGCGGACAAAGTGAATTTCCCGATCTCTTCGGCGACTCCATGGGGTGGTCCGGAGTCCCG  
GGCGCCACCGCGAGGTAAACCTCGTCTCACTCCCATACGCGACCGGGTATCCAGTTCGGCAACAGCCACCACTC  
CCGACGACCCNCGTGTGACGCGGCTGGGTTCACNCGAATAAGTGGCTCANGGCATCGTCCGGCGCGGTCCNCAAC  
GCA

## Clone Rv330

.....:Rv330SP6.seq:.....  
CTCAAGCTTGAGGTTAACTTTGAACGGATCGAGCTGGACGTTTCGAGACGGTGATCGGGCCGAACCTGAATTTGTCGGT  
AATGCCCAACGCAAAAAGCAGGGTGGTGGCCGGGCGGTGAACCGCGCTCGCGCGCACCTCGAAATCTATGTGGAT  
TGCCGGGATGGGGATGTCCGCGACCGCGAAACCGTAGTTCTGCTTGTCCCGTGAGGCCACGGTGGATGGGGGAAAGAT  
CTTGGTGTCCGGGATAATAATGGGGCCGATGCCCGGGTTGAAGTCCACTGGATCGGGAAATCCGGAATCTTGATCCG  
ACGTTTCAGCGCAACAGGCCCTC

.....:Rv330T7.seq:.....  
CGGCGACGTCGCGGATACGCCGAGCAGTTGGGAATCGCTCTGACGAAACCAATATTCTGCGCGACGTTTCGAGAGGACT  
TTTTGAATGGACGGATCTACCTGCGCCGCGACGAGCTGGACCGATTAGCGGTACGCCCTCCGCCCTGGACGACACCGGG  
CACTCGATACCCCCGACGCGAGCGGCTCGCGGCTGCTGCGGTTTCAGTCCGACCGCGCCGACACTGGTNTTCGCTGG  
GACTGCGGCTGATTCCACACCTCGACCCGCGCAGCGCTGCTGCTGTCGCGCCATGTCTGGCATCTACCGCCGTCAGC  
TCGCCCTTGATCAGAGCATCGCGCGCGGTGCTTA

## Clone Rv331

.....:Rv331SP6.seq:.....  
CTATAAATACTCAAGCTTGATGCCCGGAAACCGAGCGTGAGCAGCGCCGACGCCACCAACCGCGGGTTCGGGCGCGG  
GGCCCGGGCGCCAGGCTGCTCCGCTCGGTGATGGCAGCCACCGCGACACCAACCGGNTGCGCTACGTCNAGCCATA  
CGGGCGGAGCTACATCGGCTCGGCGGCCCACTGTTTCGGGCCCTCTTTCGAGGTCNAGGTCNATACCGATTTCGCGCAT  
CCGACGCGCACCTCGAANCANAAACCGTGCCCTACTATTGCTTGTGTCGCGGGGGCCAAAAACAGCTTGGCATCTT  
CGCCNATTTGCCGCGCGCG

.....:Rv331T7.seq:.....  
CTTCGGTTCGAGTGTGCGAGTGATAGATGACGACCGGACCTCGTCGGCATCTTCCATAGCCCGCCACACCTTCAGTT  
GCTCACCGGAATCCAAACCGTAGAAGGTGCGGAGCGCTCGGCATTGGTCATCGGATATGCGCTCGGGACGGTCA  
AGCCCTCGGGTTCGGGCCACACTCCGAGGCTTCGTGCGGGTGGTCCGACGCGCATGGGCCACCATCGCATTACCA  
GGTCTGCGCGAATCNCANACGTANACNGTTCCTTTCCCTAA

## Clone Rv333

.....:Rv333SP6.seq:.....  
CTGGCACCAAGGCCCCACAGCTCACCTGTGACCTTCCTGCGCGACCCCGCCGAGGTCTCGGCCGTTACCAACCGAAC  
GGCGGAGCGGGAGTCTGTGTCGATCGAACAANAGCAAGGTGATGGCGGAGTGTGTTCCGCGACTTCGTCGATGA  
CGGGGTCTNATCCATTTCGAGTCCGTGCGCGCTCGGTGTCGAGTGGCGTCACTCCAGGATCTCGACCTCACAGACNA  
AAGGACTTCNATCCATCTAGGTGTGGACNAACAGATCTTCTGTCCGACNACTACACCAACCAACGAGGCATCGCGCG  
CGCGCGCATGCGCAACTTCGAGCGCGTATGCGCCCGCGCGGGGGCGCTCCCCGGTTGTCAACACTTGCCGTGTTCT  
TCACGCTGTCGCCACATCAACCCCAACG

## Clone Rv334

.....:Rv334T7.seq:.....  
GTTCTTGGGCCCATGCGGAGGATCGCGGTTTCACCAACCGCGTTCGGGTGGCGTTGATAGCTACCGATGGTCCG  
CTTGTGACGCGCCCGGATACCCGAGTCCGCGTAAACCATCTTGTGCTCG

## Clone Rv335

.....Rv335SP6.seq.....  
CAATACTCAAGCTTTGGCGTGCCTTCCAACCCGAATTGGCTTTCGGCGCCATCGGTGAGGACGGCGTGC GG GTGTCTCA  
ACNACNACGTGCTCCGCGGGACACACTCGATGCTGCCGCCATGGACGCGGTGGAACGCAAGCAGCTGATCGAGCTAC  
AAGCGCGCGGGAACGCTTCGCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATC

## .....Rv335T7.seq.....

CNTCATGATGATCATACCCGAAGTGTGGTAGCCGCAGTGGTATCTGTGGGTACCGTCTGTCTTCCATGGGCGCTC  
TTTCGGGCTTTCCGTATTGGTCTGGCAGGACATTCGGGTATCGAGTTGTACTGGATGGTGTGGCGATGTCGGTGAT  
CCTGCTCCTGGCGGTGGGATCCGATACAATCTGCTGCTGATTCCCGGTTGAAAGAGGAAATTTGGGCGCGGATTGAA  
CACCAGAAATATCCGTGCCATGGCTGGTACCGGGGGAGTGGTGACGGCTGCCGCGATGGTGTTCGCGCTTACCATGTC  
GTTGTTGTGTTCAGCGATTTCGCAATTATGGTTCAGATCGGTACCA

## Clone Rv336

.....Rv336SP6.seq.....  
ATACTCAAGCTTTTACCGGTGATCGCNCATCACCTGGTTCATGAACGGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCA  
ACATGAGCCACGCTCTCGTCGGCGGTGCGGTGCAGGTGCTCGGCGAGCTCGGCCGNACAGCCGCTGACCCGTGAAC  
CAGCTTCCATATCCCGCGANNAACGACGCCAGTCCGCTACGTNACCCCTCCGCGACTGTCATGGACAAACAGCGCGTT  
CTCCACCGACCGGGCCGCGGTGGGGTNTT

## .....Rv336T7.seq.....

GCTGGTAGAGTTCGCTGACCGGTGCAGGTTTCGACAATGTGGTGCCGGTTCGGCGGCTACGTGCCATCGAGACACTGGC  
GCAGGCTATCGCAACCCGTTATCGGCTACGAGCAATCGCGGTATGCGTTCTTGAGCATGAGTCGGCGACCGTCGTCTAT  
GGTCGACACCCACGACGGAAGACGCGAGTCCGCGTCAAGCATGTGTGCCGCGGATTATCAGGACTGACCTCCTGGCT  
GACCGGCATGTTGGTCGCGATGCCTGGCG

## Clone Rv337

.....Rv337SP6.seq.....  
GCTTTCCGCGCATACCCGCCATGTCNCGACATCCAGGACTTCTGGGGGATCCGCTGACAGCGCGGGGATCCCAAAG  
TGCGGATGATCGGGCGCGCTACGTCTGTGGTGTACTCGTCCGTAACAACGAAACGGAAGCGATGACTCGGTCACGCG  
GGTGCGGCACATGGTGGACACACACCGCCACCGCGGGGTGAAGGCTTATGTCAACCGTCCGGCANCACCTCAATGC  
CGACCAAGCCGAGGCGGGANACAAANNTATCGCTAAGGTACCGGCATACNAGCATGGTGATCGCAGCAATGTTGCT  
AGTGATCTATCGCTCCGTAATTA

## .....Rv337T7.seq.....

CTTCCAACCCGAATTGGCTTTCCGGCGCATCGGTGAGGACGGCGTGC GG GTGTCTCAACGACGACGTCGTCCGCGGGAC  
ACACTCGATGCTCGCGCATGGACGCGGTGGAACGCAAGCAGCTGATCGAGTCAACACGCCGCGGGAAACGCTTCGG  
CCGCGGGCGTGAACGCATCCGTTGACCGGGCGGATCGCGGTGATCGTCGATAGGCGATCGCCACCGGACGACGCG  
CAAGGCGCGGTGCCANGTGCCCGGGCGACGGTSCGGACAAGGTGGTGTGGCGGTCCGATCGCGCCA

## Clone Rv338

.....Rv338SP6.seq.....  
TACTCAAGCTTCGCGAGATCCGGATGGCACTCAGCTGGACAAGACCTTACAAAATCTGAAATCTGACCCGATACCT  
TGAACCTGGTCTCGTTCCGCAATACTCGTTCCGGCTGCGAGGACGCGGCGCAACGCTNCTTCGCGATCAACGCTCCG  
ANCTGAATTGGCAGCAAGCGCGCTGCTGGCCGCGATGGTGAATCNACGACGCTCAACCCGTA

## .....Rv338T7.seq.....

CCCACGACTTCTCTCGATCAGTTGGATTGTACGAAGAGGCAACGAAAGCAGTGATCCTCGGGATGGTGCAGCGCT  
ACATCGACCCCGCTTTCAGCGCGCACAGCTCTGATAGTGGCTGGGCGAGCAGGTCCCAAGATTCCGCGCTAAGGCA  
GGCGTCTGTTCCGTCGGGATCGCATTCGCGCTCGGCGCTCTGCTCCCATCGATAGGAGGCTGGGCGCTCGCTC  
GGCAGGGGCTACGCGCTACCCCGTCAAG

## Clone Rv339

.....Rv339SP6.seq.....  
CTCAAGCTTATGGCGCGCGCGGAGGTCTGCTCAGGCAACCCCTGAAGTTTAGGGGACNACCTACTCAGCGCAAAAT  
TTCGCTAATTGTAGTTCGCGCCACAGGGGANANATCAACCCATGTGATCATGATCTACCCGGATACCGGATTGGCGG  
TAGCGCCACGATCGTCAAAATNTCCGCTGAATCATCGGATAGCTGATCCGCGCTCAACGCGTTTTGANTCACC GG  
GCAACAGCGCGCAGGCGCGCCGANCANCGATCTCNTGGGCGCATGGGCCCCAATCTTNTCG

0367346.110000  
:::Rv339T7.seq:::  
GTGTGTGGTGGAAACCATCTGAGCAGTGTGCCAAACCGGGGCAGACAGCTCCCAATTGACGTGAGCCCGCTCACTTGC  
TGGGTAAAGCGTC

## Clone Rv33

:::Rv33SP6.seq:::  
CTTTACACTTCCTGCATCCGGCTCGTATGTTGTGTGGAATTGTGACGGGATAACAATTTACACAGGAAACAGCTATG  
ACCATGATTACGCCAAGCTATTAGGTGACATATAGAATACTCAAGCTTGGGCGTGACGGCCACCGGGGCCACTCCG  
CACCATCTGTACCCGACCAAGATCTAC

0367346.110000  
:::Rv33T7.seq:::  
CAGGCATGCAAGCTTTAGCTGCCCGAATGCGTCAACCCGATGCGCCAGATCGGGGCTTCGCAGATAAAGCAGCAACA  
GGCGGGCAAAACGTGNATCTCGGAGCCGGAAGGGCAATCAGCCGACCGTCGACGAACGACACCGGCGAGACCACTTAG  
GCACTGACGGCCGGCCGCAACATTACGCGCTCGTTGATTAGCGCTTCGGTCTCGTCCGCGGTTCATGCCAGCAGCTTG  
CGGAGATCTGAACGCTGTCTGTCCGGGCAGCGCGCGGGCGTTGGGGTGCTGCCCGAATGTGACGAACGAGC  
CGGACCGTCTCGCGGGCCGCGGACGGCGATCCGC

## Clone Rv340

0367346.110000  
:::Rv340SP6.seq:::  
CNCAGCTTGGCGATGTTACCCCTGACAGCCTGAACATATGTCAAAACACACGGCACCGGAACGGTGTGGGGGACCCC  
ATCGANTTCGAGTCGCTGGCGGCCACTTATGGCTGGGTAAAGGCCAGGGCNANAGCCCGTGCCTATTGGGTTCGCTC  
AAACACCACTCGCCACCTGGAGGCGGCCGCGGTGTGGTGGATNCATCAAGGCGGTGCTGGCGGTGCAACGTGGG  
CACATTCCCGCAACTTGCACTTCAACCCGGTGGAAACCGGCCATCAGCGGTGGCNACGGCGGTGTCGTGCNACC  
NAAACCCCCCGTGGCGGGCGC

0367346.110000  
:::Rv340T7.seq:::  
GGAAACCGGTAACCAAGATCAGCTCGTGCACCTCACTGCCGGGGTGAATTCACCACCGGTGCTGCGCGCTGCCAGTAG  
TGCACCTTCTTGACGCTCGAAAAGGGGAGTCGCTCGGGTAGGTACCGTCAGGAGCCGCTACCCAGGTTGGCGCNA  
TAGCCGCTCTCTCGAGTATCTCCGACACGCCGCCACCGGTGCGGTCTCACCCANATCACTTTGCCCTTGGGCGAG  
GACCATCTGCTGATNCNGGGCGGTGAATGACAAAGATCTCGACCGGCCCTTCN

## Clone Rv341

0367346.110000  
:::Rv341SP6.seq:::  
TACTCAAGCTTCAGAACAGCGCTGTTGTGGGCNACCCGGCTCGCCGAGTTCTGCACGCACCGGCTCAAGTGCGGCCC  
GCACCGCCGGCATCTCCCGGTACGCAAGGCGCGGGCCGCGCCGCGCAGCGACGCGCTGTTCGGCGAGTTCCCGCTCAA  
TGATGCTGACCTGATCGGCCACCCGGCGTTCTTCGCGGTGCTGCGGTTCACTAATCGCGGTGCTCAGCAGCGTCTCGA  
CAGCACCAACCCGAGTGGCGGACGAGCTG

0367346.110000  
:::Rv341T7.seq:::  
TAATGTCTTGCCACGCTCACCACAAATCGCGATGAATTCATCATGCCGCCAGGGCGGCCAACCCAATGGTGGCCGG  
AGCGGCGAGCTCGATCGCAGCGCGGAGGTTGCCGGCCGCGAGTTGATTCAGCAACAGGGTAGGCTATAGCGGGCAGG  
ATAGTGACGAAGGCAAGACCTATATCTGCCGTGGAAGAAGATCGAGTAGCCGGTGCACACAACGGAAGCGAAAGTG  
TCCGCGATGTTGATGAGCGTCGCGGTTGTGGCGCGCGTGGCGG

## Clone Rv343

0367346.110000  
:::Rv343SP6.seq:::  
TACTCAAGCTTTCGTGAGTTCATCGCGCCAGCAGACCAACAAGAGCATCGGGACATACGGAGTCAACTACCCGGCCAA  
CGGTGATTCTTGGCGCCCGCTGACGGCGGCAACGACGCCAGCGACCAATCAGCANATGCCAGCGGTGCCGGGC  
CAGGAGTTGGTGCTCGCGGGTACTCCAGGGTGGCGCGTGATCGACATCTGACCCGCGCACCACACTGCCCGGCT  
CGGGTTCAGCAGCCGTTGCCGCCCGCAGCGGANNATACATCGCCGCGATGCCCTGTTT

0367346.110000  
:::Rv343T7.seq:::  
CCACCCGTGTAATTTGGGATGGGCGAAGGCAAGCACCAGCGTGGCCACGAACCGGGGAGGACAATCTCGGGCGG  
CTAGGGCTTCTCGCGGGAAGGCCGAAACGTCAGCGGTTTCAACACGTGCGGTGCGCTCCGACCGCGGAACATTTCGGG  
ATGCGACCACTGCTAGCACCTCGCGGGCGATGATCTCAGCGGTGACCCGCGGTAGTCGCGCGCGGGCGGCTAC  
AGTCTGAACCGGATGACCATCGATGTGTGGATGACGATCCGAG

## Clone Rv344

.....Rv344SP6.seq.....  
TCAAGCTTTAGCTGCCGGAATCCGTCAACCCGATGCNCCCAGATCGGGGCTTCGCANATAAAGCACNAACAGGCGGGC  
AAACGCTCNAATCTCGGAGCCGGAAGGGCAATCANCAGCGCTCNACAAACGACACCGCGANACCCTTAGGCAGTGA  
CGCGCGGGCCGAACATTACNCGCTCTGTTGATTAGCGTTTCGGTCTCGTCCGCGGTCATGCCGAGCAGCTTGGCGCANA  
TCTGAACGCTCTCTCTGCCGGGCAGCGCGCCGGCGGCTGGGGTGCCTGCGGAATGTGACNAAACGGAGCCGACCCN  
TCTCGGC

.....Rv344T7.seq.....  
CCGGGGCCACTCCGCACAATCNGTACCNACCAANATCTACACCATCGAATAAGACGGCGTCCGCCGANTTTCCGCGGT  
ACCCGCTCAACTTTGTGTCGACCTCAAGCCCATTCGCGGCACCTACTACGTGCACTCCAACACTTTCATCCTGACGC  
CGGAACAATNAGCGNTCGGTTCCGCTGACCAATACGGTCCGTTCC

## Clone Rv346

.....Rv346SP6.seq.....  
NCTGGCCTTTGGTCCACACTAANACAATACTCAAGCTTCGGGCGCAGAGCCGCCAACTCAGCATATCGTTAACCGAT  
ATCCCGAGCCGATAGCTGGCGGGCTCGGGTGGTGGCCAGCGCGCTGCGACNAAAGTGTGACCGTCATGAACAGAC  
ACCAACCGCGGGCGTGGCGGCTCGTCACTGCTCGANATCTCAGCATCCGACGCGGGTGTGATCGCGCTTTCCGCGTG  
TNGTGGGTCNCCGCCCGAGCCCGGCAAGCGCGGCCACACAACCCCGGAA

.....Rv346T7.seq.....  
CATCTGCCACCAACAGGACCGCGGTGGGACCGCGCTGACGCGCTGGTGGTCAGCATCGTGGCGGCTGCTGTTG  
TATGCCAGCTTCCCGCCGCGCAACTCTGTTGGTGGCGCGCGGTGGTTCGCGCTCGCATTCGCTGGCTGGGTGCTGACCCAC  
CGCGCGACGACACCGTGGGTGGGCTGGGCTACGGCTGCTATTTCGGCGCTGGTGTTCACGTCTCGTTGTTGCCGTGG  
ATCGCGAGCTGTTGGGCCCCGGGCGCTGGTGGCACT

## Clone Rv347

.....Rv347SP6.seq.....  
GACAATACTCAAGCTTGACTGGCCACCCACCGGATGACCACCGACAGGCGCGCTGGTCTGATCCACTCGAACCGCCG  
GGTGTGATGTCACAGCGCGTGAANTCGTCTGCGCGCGCAGGCGCTCNAACAGGTACAGGCGCGGCGAATTGGCACC  
ACCATTTTGAATTGGACCTTGATGTACGGCCCATCGACGGCGACGCGACCTGCAGGTACTCCACCGCAAGCCCGG  
CGGGGAAATGCCCGCGGTCNCGTGGCCACGACGGCGCGANCAACCCGACACTAGGGCGCGCCNACGCGCCCC  
GACCCACNATCAGCGCATACCCGTGACGGCGCCACNAACCTGTCAACA

.....Rv347T7.seq.....  
CCTCCAACCTCGCGGGGAAGCGACNCCAGCCTACCGAGCTTGGAGTCCANGACGCGAGCGCGCGCGCTGGTCTCGGTC  
GTGGTGGCGCGCGGGTGGCGTTGGCTGGCGAACGATCTCCACCGACCGCTGCGGTTACCCAGATCTCGGCATANACG  
CGGCGCGAGCGCGGTGCGATACCGTATTCGCTCAATTGGGACCGCGTTGTGCACTTCGGCTAGCTCGGTTGCCACACCC  
CTCAGGCGTTCGACGTTGGCGGGTTTCGGCGGCCCANCAACCGCTGTCACCATGCCCGCCAAAGCGACCTGCGCGCGC  
ACCAACTCGACGACCANCATGTCGCGCTCGCGCGCGCGATACATGG

## Clone Rv348

.....Rv348SP6.seq.....  
CTCAAGCTTTTGAAGCTCGCGCGGGGCACTTCGCGGCAATTCTACTANCAGAANTCTGGCCGATACGGATCTG  
ACCGAANTCGCTCGGCTGCANCCACCCCTTATGGCGATGGCGCCGATGCGGTTACCCAGATCTTGTGCGGCTT  
GCCGACGCGACCGGTGAGTGGTCAAGTCCGGTCTACGCTTGGGCGCTTTCGGGACGCTCCGACGCTGCTCGCGGTT  
GCGCGCANAAAGCGCGGCTGGGTGGTGGCATCAGGAATGCCTCNCCGCCGCGCATGACGCGGCTGCGCGCGCA

.....Rv348T7.seq.....  
CNCAGCTTGATTGGTCTGGTTGCATTGGCCAGCTGCGGAGCGCTGGCTCACTTCAACTACGACGACCGCAACAATT  
GCCCGCTTCGGATCGGATTCGGTTGGGTTACGCGGCAATGGAGCACCAATTTCTCGGTGAATCAGACTATTCCTGAGTA  
CTTGATCATCCTCTGTCACACGCTTGGGAACCCGCGCGGCTTGCAGCTTGGAGAGCTGCGCAACGCTGTGAG  
CCAGATCCAGCGGTGTCATGGTTTCGCGGTGTGACCCGGCCAAACGGGGAAAC

## Clone Rv349

.....Rv349SP6.seq.....  
CAATACTCAAGCTTGACTGGGCGCGACCTTCGGCGGCCACCCACCGTCAACGCGCGGGAAGTCNACGTCGTCAGG  
CCATCGGCGGCTCAGGATGGATTTCGGCGCGGAGCTGTGATCGACGCGCTCGGCGACCGGAAACCTACCAAGCAGG



CCTTCTACGCCCGGATCTCGCCGGAACCGTTGTGCTGGTGGGTGTTCCNACGCCCGACATGCGCCTGGACATGCCGC  
TGGTCTACTTCTCTCTCACGG

.....Rv349T7.seq:.....

TCGACGGTTTGGCGCCTTAAATGCACTGAGGTGCTCAATTGACCCACAGCGGAAATGCCGACTATTCCGAGGCCTC  
CTTCGCCTTGGCTGCCGCGAGAGGGGCTCCGCGGGAACCGCATGCAAGTATATGACCTCGGTTTCTCGGGTGCTACCGC  
GTGCCTTGTTNANGATNANTCTCGGCGTTGGAATTTGCTCAGCCGCGCCAAATTCATCGAGCGCANATTCGTACACNTGGC  
CGCGCGGACATACGCTTCAACGCTGGAATCTGCTCCACACGACCGCCCTGTCGGGATCTGCTCACGGGTAAAGGAAC  
TTACGTGGCACTCGG

Clone Rv34

.....Rv34SP6.seq:.....

GACCACGCCAGGCTAATCACGTGACGTACCGAATACCCNTCTAGTGGTGCAGGCTCCGCTGGAAATGGCCCTGTA  
CCAACTCGCGCACCGGTGCCAG

.....Rv34T7.seq:.....

CGGCACCCGACCCTTTGAGCCCTCCGCGCTGGCCCGGTGGAACTGGCCGACGAGGACTGATCTGCTGGGCAAT  
TGGTCGATGGCACGCTGGCCGCCATCTGAAGGTCN

Clone Rv350

.....Rv350SP6.seq:.....

CTCAAGCTTGGCGTTACCCGCACTTCCGGAGGGACACCATGACACCGCCAGCCGAGCACGAGGCCAACTCCGCGA  
CGCAGGCGCGTTGGACTTGTGCTGGACAAAGGGTTTAGCCGCCGAAGCAGTGACGTACATCGGCCAAAAGCACTT  
CGCCTGTGACCCGACGCGNACCGGTGAGGCTAGGGAAGCAGGAGACATGCGCCCGCACCCGCAATGTACACGCT  
GCAAGCAACCATCGAAACCGGATGGCTATNCTACCGCCCATCGCCCGGT

.....Rv350T7.seq:.....

CATGTGCGGCACATCCAGGACTTCTGGGGGGATCCGCTGACAGCGCGGGATCCCAAAGTGCGGATGATCGGGCCGCC  
TACGTCGTGGTGTACCTCGTCGTAACACGAAACCGAAGCGTATGACTCGCTCACGCGGTGCGGCACATGGTGAC  
ACCACACCGCCACCGCACGGGGTGAAGGCTATGTACACCGTCCGCGCAGCACTCAATGCCGACACGCGCGAGGCCGGA  
GACAAAGTATCGCTAAGGTACCGCGATCACGAGCATGGTGATCGCAGCAATG

Clone Rv351

.....Rv351SP6.seq:.....

ATACTCAAGCTTCGGTACGGTGGCGGGCGTGTGCTGSCCGCGCTCGCGGCTGCGCGGCTGCGGTCTCGTTTACN  
AGCTCGCGCTGCTGACATGCGCGNAGCCTGAACGGCGCGGGATCGTGCCCACTCCCTGATCGTCGCGGGCTACA  
TAGCCGCGCTGGGAGCAGCGCCTTGCTGATCAAGCGCTACTTGACACGCGGCCATCGCTTTCATCGCGCTGGAG  
CGGTGCTGGGCATCATCGCG

.....Rv351T7.seq:.....

TGTCAAGTCCTTTCAGATCTNTTTTATGACATGACTGGAGATCTGTCTAGATTGCAGCTCCTGTGAGCGTGGGTAC  
CGGATTCAAGCCGTCGGTCAAGCCCGGTGTGACCGGCTTTGCGGCAAGTGTGCGGCTCGAGTTCCGGCATCGCGG  
CGAAGTGTGCCGACAGCATCGGTGTACGCTGCTCGTGGTGGCAAGGTGCAAGGAGTGCCTGTTTGGCAACGACGG  
TTCCAACAGTGTGGGCGGCATCCCGGCGAAGTAGACCAAGTCAGTGGTGGC

Clone Rv352

.....Rv352SP6.seq:.....

CAATACTCAAGCTTCAAAACAGGCTGTTGTGGCGCACCCGCTCGCCGAGTTCTGCAACGACCGCCTCAANTGCGG  
CCGCAACCGCGCATCTCCCGGTACGCGAGGGCCGCGGCCGCGCCGACGAGGNTGTTTCCGCGAGTTTCGCGT  
CAATGATGCTGACCTGATCGCCACCCGGGCGTTCTCGGCTGCTCNCGTTCACTAATCGCGGTGCTC

.....Rv352T7.seq:.....

TACGCTGGCGCTGGAGGGGACNNTTACAACATCCACCGCAATGCTCTTGCCCCGATCGCGCGACAGGATGACCCA  
GGACATCTTCCGCGCCGAAGTACTGGAAAAGCTCACACCGGAGTTCTGTCGACCGGTGGTGGCCTACCTGTGCACGGA  
GGAGTGTGCCGACAGCATCGGTGTACGCTGCTCGTGGTGGCAAGGTGCAAGGAGTGCCTGTTTGGCAACGACGG  
CGCCAACTTGCACAAACCGCGTGGGTACAAGATGTTGCGGCGCGGTGGGCGAGATCACCGATCTGTGCTGGTGGGA  
AATTGCTG

## Clone Rv353

.....Rv353SP6.seq:.....  
GCTTTTCCCGTCCGTGTCNNCGCTCAACCGCGGTGAGGCGGAAGCGGNTGGTTACGACTCCCTGTTTGTGATGGACCACTT  
GTACCAACTGCCCCATGTTGGGGACNCCCGACACGCCGATGCTGGAGGCTTACACGGCCCTTGGTGGCGCTGGCCACGGC  
CACCAGNCCGGCTGCNNNTGCGGCGCTTGGTGACCGCAATACCTACCCAGCCCGACCCCTGCTGGCAANATCATCAC  
CACGCTCGACGTGGTTAGCGCCGCTGACGCGATCCTCGGCATTGGAGCGCGTTGGTTGANCTGGAACA

## .....Rv353T7.seq:.....

CNGCTTTTAAATGGCCTTGACNTGGGCGNGCCGGCCACCGGGCCACTCCGCACAATCTGTACCCGACCAAGATCTAC  
ACCATCGAATACGACGGCGTCCGCGACTTTCCGCGGTACCCGCTCAACTTTGTGTGCACCTCAACGCCATTGGCCGC  
ACCTACTACGTGCACTCCAATACTTATCCTGACGCCGGAACAAATTGACGACGCGGTTCGCTGACCAATACGCGT  
GGTCCACGATGACCCGACTACTACATCCTGACGCGGAAACCTGCCGCTGCTAGAGCACTGCGATCGGTGCGGATC  
GTGGGGAACCCACTGGCGAACCTGGTTCAACCAAACTGAAGGTGATTGTTAACTGGGCTACGGCGACCCGGCCAT  
G

## Clone Rv354

.....Rv354SP6.seq:.....  
CTCAAGCTTGGCGGGAGGGTGCATGGCGACTCGGATTACCCACCANGGGGCGCAACGCGGTGTCCGCGCCCTCNA  
GCTGAACGTGTGTCGCCGCTGGAGAACCTGGCGCTGCTGCGACCCCTGGTGGCGCCATCGGCACCTTCGAGGACCT  
GGATTTCGACGCGCTGGCGGCACTGAGGTGGCGGTGGACGAGGTGTGACCCGGTTGATTGCTCGCTGGCCCTTGGCGGA  
TGCCACCTCGGCTGCTGGTGCCTGCGCGGAANACGAANTTGTGGTGGAGGCTTCTGCTGCTGCGACACCCACNA  
CGTGGTGGCACCGGGCAGCTTTAGCTGGCAT

## .....Rv354T7.seq:.....

CCGACGCGCTGCTGGCCACCAACACCGCGACGACCGTGACCCGGACCGGGGTGCCGCGCAACCGGTCTTGGCCA  
ATTGCCGCGGCAACGCGCTCGCGCGCATGGCGAACAGCAGCGGCAATTGCCGAGCATCAACACCATCACCAACCG  
TGTTAAGCCCGGCCAGCGCGCGCAGGAGATGATGCCGCTGCCCAAGTACACCCGTTGGCTGGAACGCGGTGGCCA  
GATTTGCCGCGCCGCGCGCGGTACGCTCGCACTTGGGTGTATGGAACCATGCCGACAGCACCAACCG

## Clone Rv355

.....Rv355SP6.seq:.....  
TTNACTGGCTTTGGTCCACATAGACAATACTCAAGCTTCCAGGACATCGTCATCGCGACCAAAACCGCGAGCTAGG  
TCGGCATCCGGGAAGCATCGCGACCGCTGGCGCGGAGCGCGCTGCCGCGAGGCGGATTAGCGCGGGCAAAATAGCCC  
GCCGCGGCTCCGCGCTCCGANTACGGCGCCCGGAATGGCGTACCCGCTGTTAACACGCTTGGCGGCTGGCGGCGG  
GCTTCCGCGATCAGGTGGTAAATGCCGACA

## .....Rv355T7.seq:.....

NGACGCTTCCATCCGCGCTGTTTTGGCGGGTTGGCCACAGCAGCCCGCGGTGACGGCGACGATGCTGGGCTGGT  
TGGGGCCCTGCGCCACCGGGCTTCATGCTGGTTGGCTGTCTTGGGACGATCCCGAATAGTCACCGGGATCTGGT  
GATTTGGCGGCTACCCGCGATTACCCGCGGCTCGACGAGTTTTTGGCCTGGACTACCCGCGTGGCAATCTGCT  
GAACTCGCGGCGGTGGTGGCTGGAATGTGAGCGCGCTTACCTA

## Clone Rv356

.....Rv356SP6.seq:.....  
CTTCTCTGAGTACCNCCGNTACTTTGGGATGGGTAAAAAGGCAATNCCTTTGGTCACGAACGCCGGGAGGG  
ACAATCTCGGGCGCTGGGGCTCTCGCGGGAANGCCGAATGTACGGTGTCTCGCACTTCCCNTCCCCCTCCG

## .....Rv356T7.seq:.....

GAGCATCGGACNTACCGAGTCAACTACCGGCGCAACGGTGATTCTTGGCCGCGCTGACGGCGCGAAACGAGCCNG  
CGACCACTACAGAGATGGCGAGCGCTGCCGGGCAAGAGGTTGGTGTGCGCGGCTACTCCAGGGTGGCGCNT  
GATCNACATGTCACCGCGCACCACTGCCCGCTCGGGTTACGACGCGGTGCGGCCCNAGCGGACGATCACT  
CGCGCGATCGCC

## Clone Rv357

.....Rv357SP6.seq:.....  
TACTCATGANCATCTTTAATCANNCGTTTGGCTTTTTTATTAAATCTTGCAATTTACTGCAAAGCAACAACAAAT  
CGCAAAGTCAAAAAACCGCAAAGTTGTTAAAAATAAGAGCANCACTACAAAAGGAGATAAGAAAGACACATACCT

CAGTCACTTATTATCACTAGCGCTCGCGCGAGCCGTGTAAACGAGCATAGCGAGCGAACTGGCGAGGAAGCAAAGAAG  
AACTGTTCTGTCAGATAGCTCTTACGCNCA

## Clone Rv358

:::::::::::::Rv358SP6.seq:::::::::::::  
CTCAAGCTTCAGGTCATGTGCNCCAAGCCCTGACGCTGGCCGACACGGCCACCGCCCGCGGANACNCTGCCAAGGCC  
ACCGAATACAAACGCCGCCGAGGCGTTCCGANCCAGCTGGTGACCGCCGAGCANANGCTCAAAACCTCAAGACG  
CTGCATGACCAAGCGCTTANCNCCGANCTCAGGCCAAGAAGGCCGTCAACAGGAATGCGATGGTGCTGCACCANAAAG  
ATCGCCGAGCGAACAAGCTGCTCAGCCNG

## :::::::::::::Rv358T7.seq:::::::::::::

CATGGTGGCACTGTAGCGACGTGCTGCAATCAAGGTCATGCCGACTCTGGTCAGCTCGGANCCGCTGACACCCCGCT  
AAGGCTGTCTCAGCTCGGTGCATTACCTCACCGACGGCGAACTCCCCAGCTTTACGACTATCCGGATGACGGCACCTG  
GTTGCGGGCGAATTTCATCATCAGCTTGGACGGCGCGCTACCGTCGATGGCACCAGCGGGCGGATGGCCGGGCCGG  
CGACCGATTCTGCTTCAACCTGTTGGTGAACTTGGCGAGCTATCGTGGTGGCGTGGGACCTGTGCGCATTGAGGG  
CTACTCGGCGTCCGGATGGGTGTCGTCCAGCGCCAGCAC

## Clone Rv359

:::::::::::::Rv359SP6.seq:::::::::::::  
TACTCAAGCTTGGGGTGATCGCCTTGGTCAACGGCACCGTGATCGGATCGGGGTCAACCGCAAAATGGACTGGAGC  
TTCCGCGAANTCATCGCCTATGCTCGCGGGGGTGACGCTGACCCGGGTGACNTGTTCCGGTCCGGCACGCTGCC  
ACCTGCACGCTCGTCTATCACTCNGGCCACCGGAATCATTCCCGGGCTGG

## :::::::::::::Rv359T7.seq:::::::::::::

GTTGGNGCCTCGTCGGCGAACAATTCTCGCAGGATTTCGGGATTAGCGGGACTGGTCACCAAGTTGGGTATCGGGGAAG  
GGCTGACGTTCCGCCGACGCTGTTGTTGATGGACGGCTGGTGATGTTCTGATCACGGAACCTGGCTGTAATAGCCC  
AGGGTCGCCACGCTTTCTCATCGGGCCGACCCGGCGACCGGCGACCGAGCGTGTGCGCAGGTATGCGACGATGATTTCTCGTG  
AAGTCCCCGTACCCGGAGAACT

## Clone Rv35

:::::::::::::Rv35SP6.seq:::::::::::::  
TGCTTCGGGCTCGTATGTTGTGGAAATTGTGANCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG  
CCAAGCTATTTAGGTGACACTATAGAATCTCAAGCTCCAGGTCAATGTGCGCAAGCCCTGACGCTGGCCGACCAAG  
CCACCGCCGCGGAGACGCTGCTTTGTCAACCGAATACAACAACGCCCGGAGGCGTTCCGACGCCAGCTGGTGACCG  
CCAGCAGAGCGTCAAGAGCTCAAGACGCTGCATGACCAAGGCGTTAGCGCGCAGCTCAGGCCAAGAATGCCGTGG  
AACGAATGCGATGGTGCTGCGGCATAAGATCGCCGAGCGAACAAGCTGCTCAGCGAGCTCAGGAGCGCAAGATGC  
ACGAGA

## :::::::::::::Rv35T7.seq:::::::::::::

CAGGATCGCAAGCTTCGGAGGACAGCCGTCATGGTGGCATGTAGCGACGTGTCGCAATCAAGGTCATGCCGACT  
CTGGTCAGCTCGGAGCGCTGACACCCCGCTAAGGCTGTCAGCTCGTGCAATCTACCCAGCGCGAATCCCC  
AGCTTTACGACTATCCGATGACCGCACCTGGTTGCGGGCGAACTTCATCAGCAGCTTGGACGGCGGCGTACCGTGG  
ATGGCACAGCGCGGGCGATGGCCGGGCCGGCACCGATTCTGCTTCAACTGTTGCGTGAATTTGCCGACGTCATCG  
TGGTGGCGCTGGGACCGTGCGCATTGAAGGCTACTCCGCGCTCGGATGGGTGTCGTCATCGCCA

## Clone Rv360

:::::::::::::Rv360SP6.seq:::::::::::::  
TACTCAAGCTTGGGCTGGCGTGTGGTGGTGTGCTTGGCGCGCTGGGTATCAACACCGCCACGAAATGGGGACA  
AGAAGGATTCGCTGGAGCGGTGGCTGTCCAAATCACCCTCGCCNACCTGCTACGGGCACTTCTACATCGAGCACA  
ACCGTGCCCATCAGCTCCGGGTGTCCACCGCGGAGGACCCGGCGTGGCGCGGTTGGCCNAAACGTTGTGGGANTTCC  
TGCCCGCANTGTTATCGCGCGCTTGGCT

## :::::::::::::Rv360T7.seq:::::::::::::

GGCCATCGCCACCGCNCCGCGGCGAAGCTCAAAAGGCACCTACTGGCACCAGGCCCCACAGCTCACCTGTGACCTC  
TCGGCGGACCCCGCCGAGGTCCTGGCCGTTACACCGAAGCGCGAGCGGGAGTCTGTAGTCGATCGAACAAGA  
CGAAGGTGATGGCGGAGTTGTTCCGCGACTTCGTGATGACGGGGTCGATCCATTGAGGTCCTGCGCGCGCTCGG  
TCGAGTGGCGGTCACTCGANTGACTCGACCTCAGACAGAGAGGACTCGATCCATCTAGGTGTGGACGAACAGA  
TCTTCTGTCCGACGACTACACCACCGGACCTCGC

## Clone Rv361

.....Rv361SP6.seq.....  
GCTTGC GG GTGATCGCCTTGGTCAACGGCACCGTGATCGGATCGGGGTCAACCGCNCAGATGGACTGGANCTTCGGCG  
AANTCNTCGCCTATGCTCGCGGGGGGTGACCTGACCCCGGGTGACNTGTTTCGGCTCGGGCAGGTGCCACCTGCA  
CGCTCGTCAAGACCTCNGGCCACCGGAATCATTCGGGGCTGGCTGCACNACGGGCAGNTGTCNCCCTCCAGGTG  
AAGGGCTGGSCNAACAANGCAGACCCTCCGGCAANCGGCACTCCTTTTCGTTGGCTCTTCGGCCGAATCCGGACG  
CNAACCGCACGGCG

## .....Rv361T7.seq.....

GTTCTCGCAGGATTCGGGATTAGCGGGACTGGTCACCACTGGGTATGCGGGAAGGCGCTGACGTTTCGGCGCGATTA  
GCTGTTTGATGGACCGGCTGGTATGTCCTGATCACGGAATGGCTGTAATANCCAGGGTCGCCNCGCTTTCATCCG  
GGCCCGGACCCGGCGCACCGAGCGTGTGCGCGAGGTATGCGACGTGATTTTCGCTGAAGTCCCGTACCCGGAGAAT  
CGAACAGCTGAGGCGCTCGTCAACCGTGTNNCGGCGACCAGCGCGCGGAGCAACTGCGCAAAATGTTAAGANAG  
TCGAATCGTTGAAATTCGGCACCACTGCACC

## Clone Rv363

.....Rv363SP6.seq.....  
CACAAAGCAATACTCAAGCTTCAGGTCAATGTGCNCCAAAGCCCTGACGCTGGCCGACCGACGCCACCGCCCGCGANAC  
GCTGCCAAGGCCACCGAATACAACAACCGCGCGGAGGCGTTCGACGCCAGCTGGTGACCGCGAGCANANCGTCNA  
AACCTCAAGACGCTGATGACCGAGCGCTTANCGCCNACGCTCAGGCCAAGAGGCGCTGCAACGAATGCGATGGT  
CTGCAGCANANATCGCGCANCAACCAAGTCTCAGCCAGCTCGAGCAG

## .....Rv363T7.seq.....

CCACCCGTGATGGTGGCACTGTAGCGACGTGCTGCAATCAAGGTGATGCCGACTCTGGTCACTCGGAGCCGCTGA  
CACCCCGCTAAGGCTGCTCAGCTCGGTGCATTAACCTCACCGACGGCGAACTCCCCAGCTTTCAGACTATTCGGATGA  
CGGCACCTGGTTCGGCGGCACTTCATCAGCAGCTTGGACGGCGCGCTACCGTCGATGGCAGCAGCGGGCGATGGC  
CGGCGCCGGCAGCGATTCTGCTTCAACCTGTTGCGTGAACTTGGC

## Clone Rv364

.....Rv364SP6.seq.....  
GCTTTTCGGCGATACCCNCAATGTCCCGCACATCCAGGACTCTGSGGGGATCCGCTGACAGCGCGGGATCCAAAG  
TGGCGGATGATCGGGCCGCTACGTCGTGGTGACTCTCGNCGTAAACAAGAACCGAANCATGACTCTGTCACCGG  
GGT

## .....Rv364T7.seq.....

CAACCCGANTTGGCTTTCGGCGCNCCTCGTGAGGAGCGCGTGGGGTGTCTCAACGACGACGCTGTCGGCGGGACACAC  
CTCGATGCTCGCGCATGGACGCGGTGCAACGCAAGACGCTGATCGATCTACNACCGCGNGNGAAGCGCTTCNGCCGC  
GGCGGTGACCGCNTCCCGTT

## Clone Rv365

.....Rv365SP6.seq.....  
GGGATGGGCAAAAGGCGAAGCACCGCGTGGCCACGACGCGCGGGAGGGACAATCTCGGGCGGCTAGGGCTTCTCGCG  
GGAAGGCGCAAGCTACGCGCTTCAACACGTCGCGTCGCCCTCCGACCGCAACATTTCGGGATGGCAGCAACCTGG  
TAGCACCTTGGCGGGCGATGATCTGCCAGCTTCCCGCGGGTAGTCCGCCCGGGCGG

## .....Rv365T7.seq.....

CAGCAGACCAACAGAGCATCGGACATACGAGTCAACTACCCGGCCACCGGTGATTTCTTGCGCGCGCTGACGGC  
GCGAAGCAGCGCAGCGACACCATTCAGCAGATGGCAGCGCTGCGGGCCAGAGGTTGCTGCTCGCGCGCTACTCC  
CACGGTT

## Clone Rv366

.....Rv366SP6.seq.....  
CTCAAGCTTGACTGGCCACCCACCGCATGACCAACGACAGCGCGGACTGTCGTACCACTCGAAGCGCGGGGTGTTT  
GA

## .....Rv366T7.seq.....

TGGTGCCCGAATGGCGAGTCCCATTTANTCGTGATTTGTTGAACAGCGACGAAACCGGTGTTGAAATGTCGCC  
TGGTTCGGGATTCCTCTCCAAGCAAGAGTAACCTGGCCCAAAATAAGTTACTCGTCTCTTGCAAGACCGCTACC

CGATGCCATTTATGTGTTTCTTACGCTCANNNTTCCGGTGCGCCATCATTTATGACCTTTGCACTGCACATTGAG  
CTTAGCAGCGCTCG

## Clone Rv367

.....Rv367T7.seq.:.....  
GAATTNGCTTTCGGCGCCATCGGCCCCAGGACCGCTGCGGGTGCTCAACGACGACGTCGTCCGCGGGACACACCTCGA  
TGCTGCCCGCATGGACGCGTGCAGCAGCAAGCAGTCGATCGAGCTACAACGCCCGCGCGGAACGCTTCGCCCGCGGGCG  
TGACCCGATCCCGTTGACCGGGCGGATCGCNGTGATCGTCGATGACGGCATCGCCACCGGAGCGACGGCCAAAGCGGC  
GTGCCAGGTGCGCCCGGGCGCACGCTGCGGACAAAGTGCTGTCGCGGTCCCGATCGGCCACAGACGACATCGTGCGCGAG  
ATTGCGCGGGTACGCCGATGAAGTGGTG

## Clone Rv368

.....Rv368SP6.seq.:.....  
TAAAGCTTTTCGTAGTTTCATNGNGCCCCGGACCAACAAAGCATCGGGACATACGGAGTCAACTACCGGCCAACGG  
TGATTTCTTGCGCCCGCTGACGGCGCNAACGACGCCAGCGACCATTCAGCAGATGGCCAGCGGTGCCGGGCCAC  
GAGGTGTGGTGCTCGGGCGCTACTCCGAGGTGCGGCGGTGATCNACATCGTCACCGCGCACCACTGCGCCGGCTCGG  
GTTCAACGACCGCTTGCCCGCGGACGGGACGATCACTGCGCGGATCGCCCTGTTGCGGAATCCCTCGGGCCGCGC  
TGCGCGGTGATGAGCGCCTGACCCCTCAATTGCGGTCCAANACCATCNACCTCTGCAACAACGCGGACCGGATTTG  
TTCGAGCGCAACCGGTGGCGANCGACCT

.....Rv368T7.seq.:.....  
CCGGGAGGGACCATCNCGGCGGCTNCGGCTTCTCTCCGGAAGGTTCTANNNTNNGCGTTTCNACNCTTCCCGTCGC  
CCTGCGACCGCGCAACATTCGGGGTATGGNNGCANCTGTNAGCATCCNGCGCGGGC

## Clone Rv369

.....Rv369SP6.seq.:.....  
CTCAAGCTTCCGCATCAGATCGCTATAGAACCAGGTGCGCGTCCCAACCGAGTGGCTGGTTCGCTTCAGACGATCGT  
TACCGGTTATCGGAATCAAACTCNCGGAACACCTGACCAACGCGCTTGATCGCTGAATCGATGCGCGCTCGCTGGG  
GCTCATCGATACCGAGTGTGCTTTTCCGACCACTTCAAGTTGCGGTACGGCGAGATTGACAAAGCGGTGAAGCCCGAG  
CCAGAGCAGGAGGATCACCNCGCAAAACGGCGGATTTGCCCG

.....Rv369T7.seq.:.....  
GCTTGGCAGCCTGCGGCTGGCGGCCCTNAGCTCTTCGATCTGGATCTCCGGACTCGAGATGCTCACTTGCCCGGCCG  
TGACGCTACCCATTGCGCGCGGACCCGACGCGCCCGGTGACCAACGAGTTGGGCTGCACGCTGACCGGCCGTCGCG  
GGTCGACGCGCGTAACGCTGACGAGCTCCGANGTCCNCTGATCCGCGACCGAGCTGCCAATGCGCGGCTGCGACGCG  
ACGTGGATGTGCCCGGGGCTAGATCGCGGGGACGAGCGAGACCGCGTCACCGAGGTATCACCTTGCCGAGTTTNG  
GCCTGCCGCAN

## Clone Rv36

.....Rv36SP6.seq.:.....  
GCTTCCCGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTNACACAGGAACAGCTATGACCATGATTACGC  
CAAGCTATCTAGGTGACATATAGAATACTCAAGCTTGAGCCATCGGGCTATCAGCTGGTTGATGTCCCG

.....Rv36T7.seq.:.....  
CAGGCATGCAAGCTTTCCTCTATACATCCGACCCAAACCGCCCGACGGCTCGGCAGAACGCTCCGCATATGGGT  
CGACGACCGCGGGTCCGACTTCTGGGCTGCCAGCGCTCGCGCAACACGCGGCTGCGAACCAGCACTCC  
TTGTGATGTCCCACTATCACCTTCGGTACGCACCAATCGACCTACGCGGCTAGCTCAGCCCGGATCTTCCAGAGC  
TCCGCCCC

## Clone Rv370

.....Rv370SP6.seq.:.....  
GCTTTTGAAGCTGCGCGGGGGCGGCTTCCCGGCAATTCTACTAGCGAGAAGTCTGGCCCGATACGGATCTGACCGA  
AGTCGCTCGGTCGACGCCACCCCTCATTTGGCGATGGCGCCGACNATGGCGCTGGACCGATCTTGTGCCGCTTGCCGA  
CGCGCAGCGGTAGGTGTCGAATTCGGTCTACGCTTGGCGCTTTCGCGACGGTCCGACGCTGGTTCGCGGTTG

::::::::::Rv370T7.seq::::::::::  
CGANCCCTGTTTCGACGGGCTACCTGAATCACCCGATNCCACCGCCGGCGGTTTCGACGCCGACAGCTGGTACCGCACCG  
GCGACGTTCGGGTGTCAGCGCAGTGGGATGCACCGCATCGTGGGACGCGAGTCGGTCGACTTGATCAAGTCGGGTG  
GATACCGGGTCGGCGCGCGGTGAATTTGAAACGCTGCTGCTCGGGCATCCGGACGTGGCGGAGGCGGCAGTCGTCCGGG  
T

## Clone Rv371

::::::::::Rv371SP6.seq::::::::::  
NAAAGCTTTGTACACCAAGTGTTCNACCAGNCGCTCCATCCGGCGAAGTGGATACTCCAGCAGGTAGCAGGTTCGCC  
ACCACGCTGGTCAGTCGCGGTTTCAGCTCGCTTTCGGCGCTGCAGCAGCCAGTCCGGGAAATAGCTGCCCTGGCG

::::::::::Rv371T7.seq::::::::::  
CGCTGCMCGCCGCGCTGGGCTGCGGTAAACCAATTACCAACAACACTTTTCGGTAGCCGAACAGCGCGCGGTACCAGCG  
AAATGGCAGCAGCCACCGCAGTCGCGCAGATCCCGCGAAGATGTGGCAGATTTTCGTGCGGTTCGAGCCGCGCAAGGCC  
AGCGTCATTGTTGCTTGGCAAGGTTGCTGGGCCCGG

## Clone Rv373

::::::::::Rv373SP6.seq::::::::::  
CTCAAGCTTCTTCTGCCCTTGGCGTTNCGGATNACATCCCGCAGCGACTCGGCTTCGGCGTCGATGTCGAAGTTCTC  
GATCAGGTTCTGGATTCAGCTTCGCGGCCATGGCACCAGTGAAGTACTCGCCGTAGCGGTCGACNAGTTTCGCGGTAGAG  
GTTTTCTGCNACNATCAGCTGCTTGGCGCCANCTTGGTGAAGTGCTCCAAATGTCCTTCCAAACCGGTCCAGCTCAGC  
CTGCGCGCGGTACGGATTCGCGCATCTCGCGCTCGCCGCCGTCGCGAACTTCGCGCCGCGCATCGGCTTGGGGGCC

::::::::::Rv373T7.seq::::::::::  
GTTCAACCTACCTACTATGCGNCAATTNCCGACACGGGTGGCATCAACACGGGCGATAAGGTGGAATTCGCTGGGG  
TGAAGCTCGGGCTGGTGGCGTCGCTGGCAATCCGCGGCAACCGCGTGTGATCGGATTCTCGTTGCCCGGCAAGACAA  
TCGGGATGCAAGCCGGGCGAGCAATTNCNCCNACACCAATCTTTGGCCGTAGAAGCTGGAGATCGAAGCCCGCGGTT  
CGGAGCGGTTGAAACCAACGGGTTTCTGCGGTTGGCGCANACCACTACGCCATACCAATC

## Clone Rv374

::::::::::Rv374SP6.seq::::::::::  
CTCAAGCTTTACGCCGACGCCGCGCTACACAACCAAGGAACGATTGCCTACTGCCGAATCGGGGAACGGTCCTCG  
CACACCTGGTTCGTGTTGGCGGAATTACTCGGACACCAAAACGTCAAGAACTACGACGCGAGTTGGACAGAATACGGC  
TCCTTGGTGGGCGCCCGATCGAGTTGGGAAGTGATATGTGCTCTGGACC

::::::::::Rv374T7.seq::::::::::  
TCCNCATGGGATAACGGGTTTAGATTTCNACACACGGCACCGTGTCTCAACAAGCCGGTCATCAGCTGGGCGGGCG  
ACAACGGTATCTACTTCAACCGGTTTCGCCCGTACAAGAAAACCACTAGGCCACCATCGAGTCCAAGAAACAACCAAC  
GGTCCGCAAGTACGCGTTTCTACTACCGCTATGACACCGCGGAGGAACGCGCGTGCTCAACCGGATGTGGAAGCTGG  
TCAACAGCCGCTCAACTACTCACCCGACCATCAAACCGATC

## Clone Rv375

::::::::::Rv375SP6.seq::::::::::  
CTCAAGCTTGGGTGTTGCCGATCACCGGAAGCCNATGATCAGCCAGTTTTCGCCGCCCGCGCATCGGGCGGTAC  
CGATCTCCGCGTCATACACCCGCGGGTAACTCGCCGACGGTGCCGGTTCGCGAGCCGAAGTGACAAACGCTGATTGAAT  
CNAGTTCCANGTCCAGCGGGT

::::::::::Rv375T7.seq::::::::::  
TNAACAGCTCGCGGACGCCACGCTGCTGCGTCGGATTGCGCGCGCGGAGATCAATTCCAGGACGCTCCCGGACAA  
TGGCGCTCTGCTGGCCCGCAACGAANGACTCGAGTCCACCCGGTCCCGGGGTGTTGTCACCTCGCGATCGCAACA  
GGTTGGCCCAACACCGCGCGTTTCTACTACCGCTATGACACCGCGGAGGAACGCGCGTGCTCAACCGGATGTGGAAGCTGG  
CGCGAGTTTCGGCGAANAAGTGGTTCGCGTGATCACTTACCATCGCGCANGATCTGCGTGTCA

## Clone Rv376

.....:Rv376SP6.seq.:.....  
GCCANCGCGGTGGCGTCGACTCCCGTTCNCGACATCATACGGTCCCGGTACTGTCCAACGCGCCGGTGGCGTAGC  
CAAACGTACGACTCTCAGTGATCCCAAGTTCGTGATCCGGCCGGTGCGCCCGCTGCGGCGGGGGCTNATNTACTTCGG  
ACTNATTATCTCATCCAAAGGACACCGGGCGGTGGCTGGAATCCCATGGTGCATCGGCCACACAN

## .....:Rv376T7.seq.:.....

CGCACTGGTATCTTCCGATACGCGGTTGATATCCGGTCTGATCTCCTGCCCTTAAGCCGGATCTCAGCAGGTCC  
CCATGCAAAAGATCCGAGGTGTCCNGATCTAGGGTCTCTGTCCTCCAGATGATGAGCAAGTCCGCC

## Clone Rv377

.....:Rv377SP6.seq.:.....  
CTCAAGCTTCGGCTCAGGCGGCGCTGCGGTAACTGCTGCTGACCGGTGCAGGTTCGCAATGTGGTCCGGTTCGGC  
GGCTACGTGCCATCAAGACACTGGCGAGGCTATCGCAACCCGTTATCGGCTACAAACAAATCGCGGTATGC

## .....:Rv377T7.seq.:.....

CATCACCTGHTTCATGAACCTGGAAGCACCGCAGCGCTTCCTTTTCGGCCGCAACATGAGCCAGCCTCTCGTCGGCGGT  
CGGGTGCAAGTGTCTCGGGCAGCTCGGCCCGCAGACGCGCCTGACCTGAAACAGCTTCCATATCCGCGACGAACGA  
CGCCAGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCTTCCACCGACCGGGCCCGGTGTGGG  
GTGT

## Clone Rv378

.....:Rv378SP6.seq.:.....  
AGCTTAGCTTCCCGCCCGCAATAGGGCTCCAGTTCATCCGGTGTGACCAGATAGGGGCCAGGGTGATACCCTGT  
CTTTGCCCTTGGCTGTCCGATGCGCAGCTGCCCCCTCCAGCATCTGCAGTCCCGTGGGACCACTGTTGAAATGG  
TATAGCCGATGATCGACC

## .....:Rv378T7.seq.:.....

CCNGAACAGAAGCGGGGTTCTACCGCGGTGTGGGCGCGCATATCGGCCCTTTTACTAAACGAACCCGATGTG  
GGCTCCGATCCGGCGCATGGCATCGACGGCGACGCCGATCGATGACCGCCAGGCTTACCACCTT

## Clone Rv379

.....:Rv379SP6.seq.:.....  
CTCAAGCTTCGCGACTCGACAGCATTCTTGACAGTTGTTTGGCTCGGCATGGTTAGCCAAGGTTCTGCGGTCCCA  
CAGATCATCTTGGTCCGGTAGCGCTCTGTCGGGTATGCTGCCGCCGGGATTCTCGCTGCTATTACTCCCCCGAAGA  
ACGCCACCGGTCCAGCC

## .....:Rv379T7.seq.:.....

GCNAGCGGTATAGCTTCCCGTCTACCGCGACCGCCAGCGAGAAGCTCGTTTTCCAGTGTGTGCGGGATTCTC  
ACGCTGCTGCTGAGTGGTGCCAGACCGCTTCCGCTTCGGGTTACAAACGAGCCGCGGGCTACGATCGTGCAGCGCTG  
AAGTTGGTGTCTCCATGGACTTGGGGATGT

## Clone Rv37

.....:Rv37SP6.seq.:.....  
GTGTGGAACGCTGAGCGGATAACAATTTACACAGGAAACAGCTNTGACCTTGATTACGCCAAGCTATTAGGTGAGG  
TATATATTAATACTAAGATTGCGGCTGAGCACATCGGCCCAAGAACCGCGGAAGGCACGCGGAACGCCCTCGGCGACA  
TGGGCGACGACCAACGCGGTGCGACTTGGGGTGTCCAGCGGATCGCGCGTCCGCA

## .....:Rv37T7.seq.:.....

CACTCTCAGTACATATGCGCGCTCTCTCTCATCGTGCCTCGGCATCGTGCAGCGCGGTGATGGCTCACCTTACC  
CAAGCCGAAGCGGAACAGAGACGTGTTCCATTATTAGGGTGTGAGCACCATAACAGATTGCTCACCAGGAATCAC  
CGAGCACCAGGAGCGATGTGAGCCAGCAGCCCATCTGGGGTGGTAGCGGGGAATACGGCTAACGCGGCTCCGGTGC  
CGCGAGCCAGCGCAGACCTTCGGCGCGGACACGGCAACACGACGACCCATAGTTGTTCTTTGCCGGATGGCGT  
GTTTGGGACATATCGGGCGCGCGCGGGCGCCGCGAGGTAGTGCTGAGGCCCATCTCGTGCAGCGGATGGCC  
CCAGCCAACCGTGTA

## Clone Rv381

.....Rv381SP6.seq.....  
CTCAAGCTTTTACGGTGATCGCGCATCACCTGGTTCATGAAGTGAAGCAGCGCAGCGCTTCTCTTTTCGGCCGCAACA  
TGAGCCANCCCTCTCGTCGGCGGTGCGGTGTCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCTGAAACCA  
CTTCCATATCCGCGCANACGAC

## .....Rv381T7.seq.....

CTCAGAAGCCGCTAGCTGGTAGAGTCGCTGACCGGTGACAGTGGCGNCAATGTGCGCTGCCGGTTCGCG

## Clone Rv382

.....Rv382SP6.seq.....  
CTCAAGCTTGGCGCTCATCAAGCGCGAACAGCAGGCGGTCGGCTGGTTCGCATGACGGGTGACGGGACCAATGACGCA  
CCCAGCGCTCGCGCAAGCCGATGTCCGGGTGGCNATNAATACCGGACCCAGCGGCCCGGGAAGCCGGCAACATGGTC  
NATCTCCACTCC

## .....Rv382T7.seq.....

ACTTCTATTTCGACTGGTGTGTGTGGCGCGATCCGACTGCCGCGCTGGTCAAGGCCGGCCAGTTGTGGGATNCCACA  
GGCAC

## Clone Rv383

.....Rv383SP6.seq.....  
GCTTGTGCTATTCCGTGGCACTGTGAGACATATGCGCGCTCCTCCTCATCGCTGCGCTCGGCATCGTCGCCGCGCGT  
CATGGCGTCAACCTACCCAGCCGAACCGAAACGAGAACGTGTTCATTATAGGGTGTGAGACCAATACCAATT  
GCTCACCAGGAACACAC

## .....Rv383T7.seq.....

CGATATTCTCGTCCGCCGCGTGTCTCGACTGGGTCGCGT

## Clone Rv384

.....Rv384SP6.seq.....  
GACCTCGGCCACCAAGCCGACGCGACCGTCGAGGTGGCGATCCGGCTTGGCGTCGACCCCGGTAAAGCAGACCACAT  
GGTCCGCGGACGGCCANCTTGCCACACGGCACTGGTAAGACTGCCCGCTCGCGCN

## .....Rv384T7.seq.....

CCGGAAGTCTAGGGGACGACCTACTCAGCGCAAAATGTGCGTAATGTGAGTCCGCCCCACAGGGCAGATCAACCCAT  
GTCGATGATGACCTACCCGGATACCGGATTGGCGGT

## Clone Rv385

.....Rv385SP6.seq.....  
AGCTTCAGTTCTCCACGACGCTTCCCAATGAATTTCCCGATCCCAATCTCGGTCAGATACAGGTGCGCATAC  
CCCTTACTTCGGNAACGCTGGGCGGATTGGCCCTGCGCGT

## .....Rv385T7.seq.....

CCGCCTACGGGTGCAACATGCATCCGAGACCGATGCTCGAGCGCGACCCCACTCGCCGATGGCCGGAACCGGCTGG  
TTACCCGGGTGGCGGCTGACC

## Clone Rv386

.....Rv386SP6.seq.....  
GCGGCTGGTTACGACTCCCTGTTTGTGATGGACCACTTCTACCAACTGCCCATGTTGGGGACGCCGACCGGATG  
CTGGAGGCTTACACGGCCCTTGGTGGCTGGCCACGGCGACCGAGCGGCTGCAACTGGGCGCNTTGGTNACCGGCAAT  
ACCTACCGGAGCCCCGACCTGCTGGCAAGATCATCACCACGCTCGACGTTGGTAGCGCCGCTCGAGCATCTCGCGG  
ATTGGAGCCGGTTGGTTTGAAGTGAACACCGCCAGCTCGGCTTCGAGTTCGGCACTTTCAGTGACCCGTTTCAN

## .....Rv386T7.seq.....

GCCTTTCGCGACAATCTGTACCCAGGACACCTCTAAAAATCGAATACGACGGCGTCGCCGACTTTCGCCGGTACCCG  
CTCAACTTTGTGTGACCCCTCAACGCTATGCGGCACTACTACGTGCACTCCAACCTACTCTGACCGCGGAA  
CAAAATTGACGACGGTTCCGCTGACCACTNNNTGTCGGTCCCACGATGACCCAGTACTACATCATTCGACCGGAGAAC



CTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGTTCAACCAAACTTGAAG  
GTGATTGTTAACTGG

## Clone Rv387

::::::::::::Rv387T7.seq::::::::::::  
GCAGACCAACAAGATGCATCGGGATCATACGCCGTCAACTACCCGGCCAAACGGTGATTCTTTGGCCGCCGCCAC

## Clone Rv388

::::::::::::Rv388SP6.seq::::::::::::  
CTCAAGCTTGCCAAAGAGACTCTGCACCAAGCNGGACGCGACCTCNAGGTGGCGATCCGGCTTGGCGTCCACCCG  
CGTAAGGCANACANATGGTTCGCGGCACGGTCAACTGCCACACGGCACTGGTAANACTGCCCGCTCGCGGTATTC  
GCGGTTGGTAAAAGCCGATGCTGCCGTTGCCGCGGGGCGGATGTTGTGCGGAGTGACAATCTGACANAGGATT  
CAGGGCGGCTGGCTGGAATTCGATGCCGCGATCGCGACACCGGATCAGATGCCAAAGTCGGTNCATCGCTCGGGTG  
CTGGGTC

::::::::::::Rv388T7.seq::::::::::::  
CCACGGCGTGGATCAAGTACCGGCCGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGCTTGATGTCGGCGTTAGCGC  
CGGATTCACACACATCCCCTTCGCAAAAGTCCGTTGGGTGCAATGATGAGCGCTTCTCCCATCGAGATAGTGGAGCA  
ACGCAATCCGTGCGGTACGGTTCGGGTCTACTCGATGTGCGCGACCTTGGCGTTGACACCATCTTTGTCATTGCGGC  
GAAAGTCGATCATCCGGTAAGCGCGCTTATGACCGCCGCTTGTGCGGGTGTAATCCGGCCATGCGCGTTGCGTC

## Clone Rv389

::::::::::::Rv389SP6.seq::::::::::::  
GGCGCTCGCTCGCGGAGATGATCGCCCGGTGCCACCCGATCCGTGCCCTCGGTGAGCGCAACGTCGTTCCGGTCC  
GGCGACCACCATGTCGATGCGCGAC

::::::::::::Rv389T7.seq::::::::::::  
GCAATCGCCTTGGCGGTCGCCGGTGTGTACCGGTGATCATCNGGNGCGGATGCTCATNCGCGCATTTGCTCNAAT  
CGTTCCCGTATGCCACCTTGACGATGTCCTTCATATGGACCACGCCGATGSCCNCGCGTCTG

## Clone Rv38

::::::::::::Rv38SP6.seq::::::::::::  
CCGGCTCGTATGTTGAGTGGAAATTTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAAG  
CTATTAGGTGACACTATAGATACTCAAGCTTCCACATCGGTATGCCAAAGCATTTGCCCGGCTATCGATTTCGGGCT  
GGCATCGCAAGGTGGACTTCTTGCTCAGCGACGAGATCCCGTGGTGGATCCGCGGCTCGCGCGGGCTCGGACCCCTG  
CATCTCGCGGCGACCCGTGACCAAGATGGCGCGCGCGGAGGACAGCTCGCGCGGGGACGCCACGCCGACTGGCCGATG  
GTGCTGGCCGCTGTCCGCAGCTCGCCGACCCCGGCGCATGACGAGAAACGGCCGCCGCTCCGTTTGACCTATGCC  
CAGCTCGCTCGGGGTCCACCTCGACGCGACCGAGACCT

::::::::::::Rv38T7.seq::::::::::::  
CGCGTCCACCGCAGCGTGAGATTGGTGGCGCATTCGTCGTGGTGTAGCTGCTGTTGGCGGCGTCCCGTATTGTGCG  
GGCCAGCTTTGTGGGGGGCGCTTCTACCCACGAGTCGCGCACTTCGCAACCGCCAGCTCGACCGCGATTACGGCG  
CGCCACACGGCCGCGGAAGCGCTCTCGCAAGCGCTTATCTTTCCGAGGTTCCAGATCTTTCCGCTACGTGGGCT  
GCTCATCGCGGGGCGGGCCGAATGATACAGGTGAGGGTAACCGGTACAATGAAGTTGGTCAGTGCTGGCCAACTG  
TGTAATGGTTGCCCGCTCGGTCACCACTGATCTTGGCAAGCGCGGAGATTCGGTTCTCGCGTCTTGGCCG  
GTGGCGGTTCCCGGTTGTCCTGGCGGTGCTGTACGTGGTGTAGTGTCTGGAATCTCTCAGTTTGGGCT

## Clone Rv390

::::::::::::Rv390SP6.seq::::::::::::  
CTCAAGCTTGCCTGGATCTGGCGGCTGAGCCTGTTCTTGGGCAACATGCGAGGGATCGCCTTTTCCACACCGCGGT  
CGGGGTGGCGTTGATAGCTCACCAGTGGTGGCTTGTGAGCGCCGCGGGATACCCCGAGTGCCGGTAAACCATCT  
TGTGCTGCAAGTTTGTGCGCGTGTATGGCGACCTTGTGCGCGTTGATCAATGACNAAGTACCCGCCATCGACATGG  
GGCGCAACGTGCGCTTGTGCTTGGCGCGACGAGTTGGCGCGCGCAGCGCAAGCGGCCAANACCAACGTC

.....Rv390T7.seq:.....  
TTTGGGATGGGCAAAAAGGGCAAGNCNCGCTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGGCTAGGGCTTCTC  
GCGGGAAGCCCCGAACGTCAGCGCTTTCAACACGTCGCGTCGCCCTCCGACC GCCGAACATTCGGGGATGGCAGCAACC  
TGGTAGCACCCCTGGCCGGGGGATGATCTGCAGCGTCGCCCGGGTAGTCGCCGCCCGGGCGGCTACAGCTCGAAACGC  
GATGACCATCGATGTGTGGATGCAGCATCCGACGCAACGGTTCTACACGGCGATATGTTGCGCTCGCTGCGCCGGTG  
GACCGGTGGGTCTATCCCGGA

## Clone Rv391

.....Rv391SP6.seq:.....  
CTCAAGCTTCGTCATAAGACCATGGTGGCGTTTCTTTACCCGTCANAGTCGGGGGCGATCCGACCCGGCTCGCATCG  
CATCATCTCTCCACGACGGCCGCTCATCAGCTTGGGCCATTTCATGTACTTGATACCCCGGCTCGGGGTAGGCCA  
CTGCNACAATTCAAACACGGTGTACACGGTGAATANTGTGNANATGGGCTCTGATCAACCGTCNCAACCCGGTTTC

.....Rv391T7.seq:.....  
GAATCTTCGCTGACCCGCTATGGGTGACGACGGGCTGGGCGCCGACACCCCACTGGCCCGGGTGTGTTTCGCCCCGA  
ACCCGGATCATGGTGAGCGAAAAGGAGATTCCGCTGTCGATGCTGGGATTGCGCACCCGCGAGGGCATCGACCGATTA  
CTCGCCACCGGGGTGCGAGAGGTGCCGAGTCCCGCTCGCTGACGCTTCCGACGATCCATCCGGCTTCGCCCGTTCGG  
GTGGCGGTAGCGCTCGATGAATCGCTCGCGGCCGCTACCAAGGTGATTCTGCTCCGTTGTGTGCGAAGTGCCTTTC  
GCGATGCTATTTCCGTTGACCTACCGGCTGGGGCGCTGACACACACCCCGGTGAGGTGTTTGTGCGAGTTGGGC  
GGAATCCGTGCTCTGGTTACAGCCCCGAATCGTCNCGGCGGTGCGCGC

## Clone Rv392

.....Rv392SP6.seq:.....  
GCAGTTGGGAATCGCTTCGACGAAACANTATTTCTGCGCGACGTCGAGAGGACTNNTTGAATGGACGGATCTACCT  
GCCGGCGGACGAGCTGGACCGATTAGCGGTACNCTCCGCTGGGACACTCCGGGGCACTCGATGACCCCGACGGACG  
CTCGCGGCACTGCTGCGGCTTCANTGCCNACCGCGCCGACACTGTGATTCGCTGGGACTCGGCGTGAATTCACACCT  
GACCCGCCGACGCGCTGCGTCTGTGGGCCATGCTGGCATCTACCGCCGTCNCGTTCGCTTGATCAGACCATCGCC  
GGCGGTGCTTACCATCGGCGATCTCTCTGTTGCGGACTGAANAANGCCCAAGTGGCGGGGCGGACGCTGNNCTTT  
CGGTAACTGCGNACCGCCCATTTGGACCGCTACCG

.....Rv392T7.seq:.....  
TTGATCTGGACGCTCTGAGACGGTGATCGNCCGAACCTGAATTTGCGGTAATGCCAGCGCAGAAAGCANGGTGGTG  
GCCGGGGCGGTGAANCCGGCTCGGCGGCCACCTCGAAGTCGATGTGGATTGCCGGAATGGGGATGTCGGGACGGCG  
AAGCGCTAGTTCCGTTGTCCGCTGAGGGCCANGTGGATGGGGGAAGGATCGTGGTGTCCGGGATGATAATGGGGCG  
ATGCCCGCGGTTGAAGTCCAGTGGATCGGGAATTCGGGAATCGTGATGCCGACGTTTCAGGCGGAACAGGCCCTCCAAG  
TTGCTCGCCACNAGATGCCGTTGCTGAAGTTGCCGACATGAGGGCGCCGTTGCCACATTGCCCGAATTGGCGAGC  
CCGGTGTGGC

## Clone Rv393

.....Rv393SP6.seq:.....  
CAGGTAGGCGCGCTCCATAAATNACTCGCGCGGCTTCGCACATCTCTGATNCATCCTTGGCGAGCAGGTCAACCGG  
CGCGTGCCTGTCNAGAGCGGTTTGGCGGTGCGAGCACTGGCCGACACTCGGGGGGTAAAGCAATCCGAGAGCAG  
GAGGACNAGTCGACGAAMCTGCCGAGCGCGTCTGACCGCTCAGGCGGATGTGCGCGGCTCCGCCACCCCGTACCGC  
CCGATCGACACCTGTATGACCCGCGGACNCTGACCTGGGTGACGCGGAGGGTTTCAGGGCATCNACNATCTCGCT  
GGCCTCGACCGCCCGGTCCAGGGTGACCGCCATCGTGGTTCCTCCGCACTTCCGGTTCTACTACCGTAAACGCTACC  
G

.....Rv393T7.seq:.....  
CGGGGAACGGTCTCGCACACTGGTTCGTGTTGGGGGAATTACTCGGACANCAAAACGTCAGAACTACGACGGCAG  
TNGGACAGAAACCGGCTCCCTGCTGGCGGCCCGCATCGATTGGGAAGCTGATATGTGCTGTGACCCCAAGCAAGGAC  
TGACATTTGCCGGCCACGCTCGACTGGAAAAGAAACGGTGATCACCGCCCGCTAGTGGACGGTGACGGCCAGGCCG  
TGCGCGCGCGGTTTCTGCGGCTGTGGGACNCTCGACGAGTTCCAGCCGCGGAGGTGCTGCGCTGCGGCCACCGGG  
CGAATTTCCGTTCTTTCGCCGCGCCCGGATCTGGGACGCGNCGCGCGCGTGT

## Clone Rv396

.....Rv396SP6.seq:.....  
CTCAAGCTTTGTCGACAAAGCGTTCGCGGGCGGTGAGCAAGCGAAGCTCGGTGCGCCATGCGGGTGCATATGCCC  
CCAGGGA  
.....Rv396T7.seq:.....

CGTCAGCAGCGCGACGTCGCGCATGCCGAGCAGTTACACAATCGCTCTGCAGCAAAACCAATATTCTGCGCGACGTTT  
GAGAGGACTTCTTGATTGGACTG

## Clone Rv39

.....:Rv39SP6.seq.:.....  
CTGCACTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTAC  
GCCAAGCTATTAGGTGACACTATAGAACTACTCAAGCTTCGCGCAGCGCGGGTTGACCCGGTTACGCCGCTCATAGC  
TGGCCAATCTGGCATCTGTCGATCANCATGTGGTGGGGGGTGACCTCGGCGGTGATCGAAATACCCCTGGTCTTATCCC  
ATTTGAGGATTCGACGGTGCCCGCGCGCGACGCGTGACAGATGTGCAACCGGCGCGGGCTCACGGGCCACGAAGG  
CGTCCGCGGCGCAGCATCGATTCTCTGGCGGGCCGCGGCCATCCGCCAGGCCAGCCGCGGCCATGGGTGCCCTCGT  
GCGCGACGCGCGCAGCGTCAGCCGGGGCTCTCGGCGTGTGGCGATCAGCAGCGCCAAACCGGTG

.....:Rv39T7.seq.:.....  
CCGACGCGCACTACGTGCTGTGTCCACCCGCGACCCGACCGGCGCAGAGTACGCAAGTACCCGATCGTCGATGGCG  
CTGTCCACCGAGGAACCTGTCAATGTGTCGAGCAGTACTGAACCGTTCCGAGAAAGSCCAGCATGAACGTCAACGAT  
CCATTCCGACCATCTCTGCGGCCCCACACCGCGCGCAGAAAGTGTCTCGGCCAGCGGCATGACTTTGGGTGCCGTC  
TCAGCGCACTGGAGGCGCAGTATTTCGGGCATTTCGAGCGCGCTGATGGACCGCTTCTCCCGAGGTAAAGTTGACCAAG  
TCGTGAACATCTAGCTCAACGACGAGAAGCTGCGGTTCTCCGGCGGCTCCGACCCGCGATCGCTGACGGTACTCGG  
TCACCATCTCCCCCGCTGGCCGGTGGGTGAGCGGACACATGACACGATACGATCTACTGTTGCATGCCTTG

## Clone Rv3

.....:Rv3SP6.seq.:.....  
TGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG  
CCAAGCTATTAGGTGACACTATAGAACTACTCAAGCTTCGCGGAGGGTGATGGCCGATCGGATTTACACACCAAG  
GGCGCCCAACGCGGTGTCGCGGCCCTCGAGCTGAACGTTGCTGCCCGCTGGAGAACCTGGCGCTGCTCGGCAACCTG  
TCGCGCGCATTCGCGACCTTCGAGGACCTGGATTTCGACGCGCTGGCGACCTGAGGTGGCGGTGGACGANGTGTGC  
ACCCGGTTGATTCGCTGCGCTTGGCGGATGCCACCTGCGCTGGTGGTCATCCGCGAAAGACGAAGTTGTGGTG  
GAGGCTTCTGCTGCTGCGCACCCACGACCTGGTGGCACGGGCGAGCTTTAGCTGGCATCTCT

.....:Rv3T7.seq.:.....  
GGAAACACCGNCGCGCTCTGGCCACCAACCCGCGACAGCACCGTGACCCGGACCGGGTGCCGCGCAACCGGT  
TTGGCCAATTTCGCGCGGACCAAGCGCTCGCGCGCATGGCGAACAGCAGCGCGCATTTGCCGAGCATCAACACCATC  
ACCACCGTGTAAAGCCCGGCGAGCGCGCGGACGAGATGATGCCGCTGGCCAGTACACCCGTTGGCTGGACCGCG  
GTGGCGCAGATTTGCCGCGCCGCGCGCCGTTACGGTTCGCAAGTTGGGTGTATGGAAACATGCCGACGACCAACCGAT  
ACCAGCAGCTAGAGAAGGGTCACGACCCCAACGCGACGCGAGAATCCCTCGAGGAGCGTCTCGTTGAGGACGCTTGTGTC  
TCTCGGCCATGTGGCCACGATGTCAAACCCGATAAACCGCAAGAACAGCATGATCGGCGGACGACCGGCA

## Clone Rv40

.....:Rv40SP6.seq.:.....  
CCTGCTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTA  
CGCAAGCTATTAGGTGACACTATAGAACTACTCAAGCTTGTCTCGGCGGTGGCTCGGCCAAGAAATCGTCGACGCG  
CGGCTCCTGTGCAATCGCTTGGCGGTGCGCGGGTTGTCAACGGTGATCATCAGGTCGGGATGCTATTTCGGCGCA  
TTTCTGTCGAAAGCTTCCCTGATGCCACCTTGACGATGTCTTTCAGATGGACGACCGCGATGGCCCGCGCGCTGCTGT  
TATCGTCTCATTTCCGCAAGCATTAGGGGTGTCCCCCGCGGAGCTGATGCGCTGACAATGGCACCCACCTCTCTCAG  
TGGGTTGGCCACCGTGATGCAAAACCACTTCATCACCGCAGCGCGCACCTTTCGGATCCGAACGGATGCGCTC

## .....:Rv40T7.seq.:.....

TTCTGTCGATGGCGCGCGCGGCTACGGTTGACCTGTGGGTGTGCAATTGGGGTCAAATTCGAGGTGCGCGCGCT  
AAGAGTGGTCTATCTGACCGCGCGGGGGCGAAGCTGCGCGGCTCACACCGCGCAACACCGACAGCTGCTGTTGGA  
CGGCTTGGCTGGGATATCCGCGCGCATGACGAGCAGCAGCAATTCCGCGAGCTGTGGCTTCCCGGGTGGCGAAGT  
GCTGTGCTGTGCAACCTGTTGATGAGGCATACATCACAGCGGGGCGCGCGCATGCAAGGATGCGCGCTGCTGCT  
CGACGACCGCGGCTGGGACTGCGCTGGCGCAAGAACTTCGCGCTACTCTGCGATCTCGACCAAGCANGTTGGCG  
CATGTGCTGACGCGGATGACTTCAACGAATCCCTCCGACACGCGCAACGAAGTGTCTGTTGGTGTGCTATGC

## Clone Rv412

.....:Rv412SP6.seq.:.....  
GCGGCGAGTGTGGTGGGTGCGCAACGCAATCCAACGACGCACTGGCGGAGAGATACCACTTGTCTGTAAGCAAC  
GTGCTGATGATCTCCCGTGGAAATGTGCTCGCCGCGCTTATCGAAACAGTAGCATGCTGCG

::::::::::Rv412T7.seq::::::::::  
CAACCGCGCTCGGCGCGTCTGGGCGCTTCGCGCGGCTCCGCCGACAATTCTATCTCTGGATCAGCGGGGCTCTCCGGGC  
CGGCCTCCGCGAACTCAACAGGCGCGCGCTTCGCGCGGAAACATTCCCTAGCCATATATGATCGCACCTCGATACACG  
ATCTGGCGGAACACCGCAAGCGTCCGACGGGCCAACCTCCGCAATTACGGTATCCGGG

## Clone Rv413

::::::::::Rv413SP6.seq::::::::::  
GAAGGTCCGCGAAGGTGTGGCTGGNTGCCGATCAGGAATCCAATGATGCAGTGGTCGGAAGATATTAGCCACTTGCTG  
TTCTGGAGACAGTCTGATGATCTCCCGTGAATGTCCCTCGACTCCGCTCTATCGAAATCTGTGAACA

::::::::::Rv413T7.seq::::::::::  
TCCTCGCGCTCTGGGCCATTCTCGGGTCTGCCGACAATTCTATCTCTGGATCTGTGGGGCTCTCTTGGCCGGCCTCNGC  
GATCTCTTCANGCGCGCCTTCGCGCGAAACATTCCTATCCATATATGATCGCACCTCTATACACGTTTGGCGGC  
AACACCGCAAAGTGTCTGTGC

## Clone Rv414

::::::::::Rv414SP6.seq::::::::::  
AGCTTTAGCTTGGCGTATCAGCGTGGGGCGCGTGCCTATTTCGGTCCGCCAACCGGTTGCCAGCTCCCTCGCGTGTCA  
GGGCTTGGCGCCAAACTGGCCACCGCAACAACTTTGGCTGAGCTTGATC

::::::::::Rv414T7.seq::::::::::  
CTCTATCTGGCGTCACTTCGCAATCTTTAGATTGCAGATATCGATAAAATCACCCGCGGACAAGACCGCATGTCA  
TCCTTTCGATGTTATTTCCCGGCGCTGGGGAAGCGCAACGACGTTGCCTACACGTTCCGCCGT

## Clone Rv415

::::::::::Rv415SP6.seq::::::::::  
AGCTTTNCTTGCATCTGCACCCCGATCCACGTGAGCCACGTGGCGTTCTCCACCAAGAAGTTGGCGGCATTCTCCT  
TGCCCTCGCCGAGCTGCTCGCCCTCTGAGGTGAACACGGCACCCGACTTCGGGATGAGGCCCTGATCCACACCCATGT  
CGATCAGCGAGCCCTCCCTGTGATTCCTTGGCGTAGAGGATGTGCAACTCGGCCCTGCTTGAAGGGGGCGAACAAT  
TGTGCACGACAACCCCTTCGGCGACGAGGGTGTGAGTTCTTCGACCTCGAGGTGCAACGTTCTGTCCCGCGCGGTTG  
CGAGCACTTCTCGGATCAGGAATAGCGGANTTCTTCGCCACGATGTGCTGACGGAATTTGTATCCAGGGCATCCG  
CGAGCGCTGCACGGC

::::::::::Rv415T7.seq::::::::::  
ACTGTNAGGGGAATGCTTCGACGATCTACCTGCAGTCGCTTGTGCATAAGCGGACGGCCCNACCTGTTCTGTTTCCG  
GGACACGAGACGGCGGAGCACCAGCGATACGGCGAAAGGTTTGAGCGGAAGGAGTTGCGCAAAATCGGGGCGCCCAAC  
ACCCGTCGCGAAGACGGCTCAAGCAGCTGTTTTCAGGCGATCAGGGTCACCGACTCAGCTGCACTGAGAACAAAGCGAT  
CTGCTGATCTGCCAGAAGATGACATGAATGTCCACGGCAAGCGTATGGCCTGCCGCTCTTCGGGGAATGTTTGGC

## Clone Rv416

::::::::::Rv416SP6.seq::::::::::  
TGAATTATGATCCCGACACAACCTGCATCANTTTAGCGCGCTCGNGATGCTATCCGCCGACGGTTTGGANCNGGTCGGT  
GTCGTTTCGTTGATCTCACCAGAGTTGTGTCCGCGCCGCCGGGGATCTAGCGAAGCTGGGATCGACAAATCAGCGC  
CGCCCAACAGCGGCGACGGCTGCGGACACGCAAGTGTGCGCGCGGGCGCCGATNAGTGTGACGCGCATCGCGGC  
GCTGTTTGTATGTACGGCTGNAATATCCGCGCATCAGTGCAGAGTTTCCGCGTATCACCANCAGTCCGTGACG

::::::::::Rv416T7.seq::::::::::  
AACGGGAGCCNCAAGAAACCATCAANAACGAGGGGTGTCACCAACGTGCAAAACCGAGGTTGCCAGCGGCGCCACG  
ATATTGCGTGTCTGAGGGTCCGCTGTACCTCTCACCAGACGTGAGTCCACACCCCGGAGGCGGGCGACTCTGGCTCG  
TTAGCAGCGAGCTCAAGGTGTCCGCGACCACTGTCTCGAATGCTTTAAACGACCGGATCAGCTCTCCGCGGATCTA  
CGTGAACGAGTGCTTGGCAGCGCCAGCGACTGGGCTATGCGCGGACCGGATCCGTTGGCGGATCGTTTGGGACCGC  
AAAGCCGGTGGCGT

## Clone Rv417

:::::::::::::Rv417SP6.seq:::::::::::::  
AGCTTTGGAGCCNCNCCGANCNCNCGGTACGCCCGCCACCGCGTACCCGGCACCAGCCCTTTGAGCCGTTTCGCC  
GTGGCCCGCGTGGANCTGGCCGACGAGGGACTGATCGTGTGGGCAAAGTGGTGCATGGCAGCTGGCCCGCATCTG  
AAGGTGCGCATGGAGATGGAGCTGACGACCATGCCGCTGTCGCCGACNACGACGGTGTGACAGCGCATCTCTACGCG  
TGGCGGATCCCATCGCGCGCCGCGACNATGCANAGCGCANCATGCTGAGGAGCGCGCCGATGAGATGAGCGCGC  
CGAACCCTTTACNCTCTGGGTGCCGATATGCAACCGTGGGGGAATGGGGTAATGACTTC

## :::::::::::::Rv417T7.seq:::::::::::::

TTCTCNATCGTTCGTACTNNGATGGGACGCTGCTGCCGAGGCGATCTGGCCAAACCGGCTCTCGCCGCGCTGACC  
TTCCGCGGGGCGAAGCTGAACCTCTTTCCGATGGGCGCTTGGGCCAAACGTACCGGGCTATCTTCATTCGCGCTCAG  
ACGAAAGATATTTCCGCTTACCCTTCGTATTACGTGCTTACGCCGCGCAGCTGGTGCAAACCATGTCAACCTCACC  
TGGTCGATCGAAGGGGCTCGGACGAACGCGGCAAGCTACGGCCACCGGTGTTGCGGATCCTGCGGTACATCACC  
GCGGTGACGAAATCGACGCTGCCGAAGTGTATTGGTGCCGACCTCGATCGTACGAACAGCTGCACGAAGTGGAA  
GCCATGACCACCGAAGCTATGCGCGCGTGAA

## Clone Rv418

:::::::::::::Rv418SP6.seq:::::::::::::  
TTCTTCGCGGTACCGCTGATCGCGCGCACCATCAGCACCCCGGTGCAGGGCGAGGCGCGCGCGTGTGGTGTGCTA  
CGCGCGCGCAGCCCGGTACCGGTGTGATCGCGGTGGTGGCGCCCGCGCGTGTGGAATGTGCGGGGGTGCACGAC  
ATCTTCGCGCAAGTCGCTGGGCGATGACAAACGCGATCAATGTGGTGACGCCACCGTGGCCGCGCTCAAGCTGCTGAC  
CTCTCGGAGGAGGTGGCGCGCGCCCGCGGTTTGCCAATAGAAGAGCTCCCGCCGCGGGATGCTG

## :::::::::::::Rv418T7.seq:::::::::::::

GTGCAAGGTGACCATCTACCTTGAGTGCCATACCGCCCGACCTATGCCTCGGATAGCTCGGCGGAAAGAAACGCT  
TGCAGTGCAGCGGAATAGCGGCTACGTGCTGAGCGCCCATCAACTCTCGCGCGGAGTGATCGCCAGCTGGGCGGCG  
CCGACGTGCAGCTGGGGATTCCGGTGGCGCGCGCGGCCAACGCGCCGATCGTGACCCGCGAGCGAGATCGGCGCGA  
TGTCGTACGCTGCATAGGCACTCCCGCGCGCTGGCAGGCCAGTTGCGAAACGCCCGCCGCGGTGCCTTCGCTCGG  
TTGGCTTTACCGCAAATTTGGGGTTGCCCT

## Clone Rv419

:::::::::::::Rv419SP6.seq:::::::::::::  
AAAGCCACGGAAGCATTTGCCCTACTGCCGAATCGGGGAACGGTCTCGCACACCTGGTTCGTGTTGCGGGAATTACTC  
GGACACAAACGTCAGAACTACGACGGCAGTTGGACAGAATACGGCTCCTGGTGGCGCCCGGATCGAGTTGGGA  
AACTGATATGTGCTTCGGACCAAGCAAGGACTGACATTCGCGGCCAGCGTCTACCTGGAATAA

## :::::::::::::Rv419T7.seq:::::::::::::

TTTCGCCACCGCNAGTCTGTCGCGCTTCAGAAAGCGTGGTTTCGCCGGGCGCGAGGATTGACGCTCAACTGACC  
AGCCGGTCCCGCCACCCGTTAGCGAGGATCGCGGTGTCTATATGTCGCCCTCGGCATAAACGCCATTTGCTGCGGTGA  
AAATCGGACATCTCGCCGATTCGCGAGTTAGCCAGCTACATGATCCGCTTTGTCCGCGCGCGGTGCTGACAAACGCGATGTCN  
GCCTCCTGGGAAGCGGTGCG

## Clone Rv41

:::::::::::::Rv41SP6.seq:::::::::::::  
TCGCCAAGTGGATTCTGTGCTACCNACGAGATCCGTGGTCCGATCCGNGCTGGCGGGGCTGCGACCTGCATCTCG  
GCGGCACCGCTGACCAAATGGCGCGCGCGAAGCAGAGCTCTCGCGGGGACGCCACCGCATGGCCGATGGCTGG  
CGCGGTGTCGCGNCGTCNCCGACCGGCCCATCNACCAAACCGCGCCCTCCGTTCTGAGACTATCCACAGTGC  
NTCGGGTCCAGCTCGACGGCAGGANAACGTAAACAGCGTCTCGANCGGTTGCCCCCGGCTTCGTTGACATCGT  
GTTGGCGCGCGCGCT

## :::::::::::::Rv41T7.seq:::::::::::::

TACCGTCACCATGATCGCCCCCATCGGATCGGTGAGCTGATAGATCCAGCCGTTTCGCCAACCCCGGAGCGATC  
TTGGCGCGCTGCTGTGTGTCNCTGANACNTAGCCACCAACAGAGCCCGGTGTGCGCAACAGAGACTGATCGGATCTCT  
CCGGAACNCTGAGGGGGTCTNCCGAGNCGCGCGCCACCCGAGGTAAAGCTCCGCGAGCTCACACGCGGACCG  
GATATCNCAAGTCGCGCAATAANCCACCACTCTCGGACCCACGTTGTATGGGCTGGT

## Clone Rv42

:::Rv42SP6.seq:::

ATACTCAAGCTTAGACCTCTACTGATGTGGCGGGACGCGGGAGATAACCGCGGTTCGAGCCGTTCAACAGTGGTGGTTC  
CCACACCAAGTGTGTTTGCCTTTGCGAAGTAAAGCGATTTCGATTGCTCGAAAGAGGGGCTGGCTGCTCGTGAGGGACAT  
CCATGGCCGATACCTCAGCGATCTCAACGGTCAAGCGACTGCATGTTTGGCGCAAGGATATCGTAACCATAGGTTCTGT  
GACGGATTTCAGACGAAGAGCTTTCCAAGATTGCTGTCCACATANTGATTCCGATCTCTACACCTTTCGCGCGGTGC  
TGTCAGAGGCACTTCGAATCAGTTATCTCGCTCGTGCTTGGAAATAATTTCCCAAGCTCGCTTGGACAAACCGCGTC  
GCCAAAGCGGT

:::Rv42T7.seq:::

AGCTTCCCAGAAACAGTGCAATTCCTAAGCAGCCGTTGTACGCGCGATGAGTGAAGAGTGACAGCAATCGCCGGAA  
TCCGGCAAGCCCTGCACAAGCGAAATCAACCCGAGGCTGACAAGGCAACGTCGGTGATCCGTACCGCTGGTGTGGA  
CAAGCGCAGAGGGCGGCTCTGTCGGTCCATCTACGCCGAGCACACTGGTGATAGCGCGCATCGGATCGTGCGGC  
CACGGTGGAGACGACGCTCCGCGGGCTGTGGGTGAGTAACCCGCCGACAGTCTTCGGGCAAGCTGTGCACCATCGG  
GCGCCACGTCTCCAACGCGCCACGCGCCATACCTGGTGCCAGTTGCTTGGCGATCGGGTGTGGCGCGCGGATCGGA  
CGTCGCAGAAACGCAACCCCGTGAGAAGTGACCAAGCGCGCTGGACACGTGCTGCGTTAC

## Clone Rv43

:::Rv43SP6.seq:::

CGGCCGGGATGTGCGCAATGGCAGGTTGTGCGCCGGCTTGATGTGCGCGTTAGCGCCGGATTCCACCAACATCCCCTTG  
CGAAGAGCCGTTGGGTGCAATGATGTANCGTTCTCCCATCGAGATAGTGAGGACAACGCAATCCGTGCGGTACGGTT  
CGGGTCTGATCTCGATGTGCGCGACCTTTGGCGTTGACACCATCTTTGTATGCGCGCGAAGTGCATCATCCGGTAAGC  
GCGTTATGACCGCGCCTTTGTGCNCGTGGTAATCGCGCCATCGCGCTTGGTCCACCGGACCGTGCAGCGGGGCG  
ACCAAGGACNCTCTCGGGGTTGACCGGGTGATCTCGCGGAAATCAGATACGATCGTCCGCGGACGACGACGCGCT  
GGGCTTGACTTGCGAATTGCCATGGTCTAATCAGGTCTTCTCTCACCTCTCGTCGCCGGGCTAGGGCGCATTCGCT  
GCTCT

:::Rv43T7.seq:::

TAGCGGTGTAACCAACTCCGGGTACCAACCCGCAAACTCTTGGCGCAACAGCACCGTCGACGCGCTCAACCGGGCTG  
CCCGGAATCTCTGGATGGGATCGAATGCAATGCTGACGACGTCCTCCGACGCGCGCGGTGGCAACGACAAGTGCGCCG  
GATCGACCAACAATGACGGCGCACACCGGTGGGACGGCGAGCAGGAGCGGTGTGCGCGAAGTCGACGCTAATGC  
CGTAGGCATTGGCCGTCAACAACGGCGACGCCCGCGGTACCAACGAGTCCACGNGGTTGGCGGTCTCTCGGCCAA  
CCAGGCGTGAACCCGGCGGATCCGAATCGACGAAGACCCGTGGGC

## Clone Rv44

:::Rv44-2ndSP6.seq:::

CCATTGTGCTGGTGTGCGCATACCAATACNACGCGCGGGCACCTGACGCGCGCGCGCAACCAATTCGGTGGCCATCGC  
ATCTGCTCGCCACCGGTCAACGGACGACCTTCTCTTGGCCGACCTAGTGCGCCCAACCCGCCGCTTGCCTCCAT  
CGATCCGGTCAACATGAGCAGCGCCCAACACGAGCGGTACATGACATCTGCTGTGGAACAGTGACANATTCGCCGCG  
CATGATGATCTCGACGCTCTCCGGATTCGCT

:::Rv44-2ndT7.seq:::

GCCGGCTCGTCAAGGGGCGTCCGAAGANCCGGGCTGGGTAACAAGTTCCTGGCTCATATCCCGGAATGCGACGCC  
ATTTGTCAAGTGGTGGGGTGTTCGTCGACGACNACGTGACTCATGTACCGGACGGGTGATCCCGAGTCCCGACAT  
GAGGTCTGTCGAGACGAGCTGATCTTCCGACATCTGCAAAACCTGGAGCGGGCCAGCGCGCGCTGGAAGAANGAAGCN  
CGCACCAACAGGCGCGCAAGCGGTTACGACCCGGC

## Clone Rv45

:::Rv45SP6.seq:::

GATCCACTGACCACGATGACATATCGAAATGCTCGACGATTCCGATGGCGATCAAGGCCACGATGCCCTGGCGGTTGG  
CGGGTATCTGGTGGATGGTGTACCCGGGTAGGTTCCCGTGATCGTGTGACCCAGTCCACGCGATGGGCGCGAGGT  
CGTCGGACGCAATCACCCCGGCTGTTCGTCGACGACNACGTGACTCATGTACCGGACGGGTGATCCCGAGTCCCGACAT  
ACCGTTGTGTCGCGCGATCTTCTTANCGTCGCCGCGTGGTCAGGAAAGTAAACAGCTCAACGGGTTTCGCGCGCTCG  
TCCGCGGGGATGACGATCTCGAATCTCGGCTGGGATCGAACAACGGACGTGCGC

:::Rv45T7.seq:::

TCTACTGCCGAATCGGGGAACGGTCTCTGCCCAACNCGGTTGCTGTTGCCGGAATTACTCAGGACACCGAAACGTCGAG  
AATACGAGCGGAGTTGGACANAAATACCGTCCNCGTGGCGCCCGCATCGANTTGGGAAGNGAATGTGCTCTGG  
ACCCACCAAGAAATGACATTGCCGGCGCCCTCAACTGGAATAGAAACNGTGATACCCGCGCGTCTTGGAAAG

GAATGGCATGCCCTGGGCGGGCGCTTCCTTCCGCTGCCGGACTCCTCCACCAATTACC GCCGAAGGCGTCCCGTCT  
GC

## Clone Rv46

.....:Rv46SP6.seq:.....  
ATACTCAAGCTTCTGTCAACCGAAATCCGCGATGGGATAACGGGTTAGATTTCGACACAGGGACCGTGTCTCAACA  
AGCCGGTCATCACTGGGCGGGCGACACGGTATCTACTTCACCGCTTTCGCCCGT

.....:Rv46T7.seq:.....  
CTGGCTCAAGCGCTCGGCGCGCAGGTGAAGTCCGACCGGCTCGAGCTGCCGGAACGCGAGGCGGTGCTGGCCACGCG  
GACGCGCTCGTCCGACATATCGGCACCGTGCACAAGTCTACAACAACGCCGCGATCGCGTACACGCGCAACGTCGACA  
AGTCGGAGTTCAAGGACATCGAGCGCATCTCGACGTCGACTCTGGGGCGTCTCCACGGGGCC

## Clone Rv47

.....:Rv47SP6.seq:.....  
CGCCCTCCGCATTATGGGTCAAGAACCATCGGTCGGACTTCTGGGCTTCAACGCTCGCGCGTCCCN

.....:Rv47T7.seq:.....  
CCGTGGCATGTGACAGATATGCGCGCTCCTCTCATCGCTGCGCTCGGCATCGTCGCCGCGGTCATGGCGTCAAC  
CTACCCAGCGCAACGCGAAGCAGAACGAGTGTCCATTATTAGGGTGTAGCACCAATACAGATTGCTCACCAGGAA  
CTCAGCGAGCACCGGACGGATGTCGCCACCAACGCCCATCTGGGGTGGTAGCGGGGAATACCCTAACGCGGCTCC  
GGTGCCG

## Clone Rv48

.....:Rv48SP6.seq:.....  
TACTCAAGCTTGTCCAAATATCGAAGCGTCGGGTCCGCGAGGCTCGGTCCGCGAGCTCAGCAAAAACCGCTCCACCCCT  
AGATGCCGGTATCCCTCAAGGTCTTTATCCGCGCTTCAACCCACTGGCACAGGTCAACGCGACGTCGCCCGCGGC  
ATGGCGCGCAACCGCTGAAGCGGACCCGACAGCGCTGCGGTGATGGACTGATCGCATCCACCGCGGATTGAGCCGG  
GCTATCCGCGGGAAGTTCCGCGGTCCCGGCCACATACAGCGGAGGATAGGGCTTTGTACCGGCTTCCGCGAGCAG  
TAGATCGGATCGAAGTCCACATATGTCCTCATGGAATCCGCTGCTCCTGCTCAGATCTCGATTATCGCGCGCAAC  
CGCTCATCGATCACAGTCCGCGCACCGAGGTTCCACACCATGTTGGCGACTTCTTCCGCGAACAGCGACACCCA  
CGCGGAACGAACCGTCCCTGCG

.....:Rv48T7.seq:.....  
CAGGCATGCAAGCTTGGCCAACTCCTCATCGGACTTGAAGGTGCCGCTCCTGTTGGCGGCCCTGCTCCACGGCAGTT  
GATGGCCACAGGAATGTGTCGGGCGGCTGGCTTTGTTCTCGCGCAGGTGCGCGGGGGCCAGGATCTTTCGGGAGAA  
CTCGTCCGGAGAGCGGACGTCGATGAGGTTCTTGACGTTGATGGCCCGCAGGACCTCGTCGCGGAATGCCGGAATCGT  
GTTATCCGCGGGGANGCGGTGTAGGAAGTCAACGGCGGCTGACCGGCTCGTGGACAGCGGGCGTCCGTGAGGCTC  
C

## Clone Rv49

.....:Rv49SP6.seq:.....  
ATACTCAAGCTTCAAAACAGGCGCTGTGTGGGCGCACCCGGCTCGCCGAGTTCTGCAGCGACCGGCTCAAGTGCGGCC  
CGCAGCGCGCATCTCCCGGTCAAGCAGGCGCGCGCGCGCGCGCAGCGGCGTGTTCGCGCAGTTCCGCGTCA  
ATGATGCTGACCTGATCGGCCACCCGGGCGTCTGGCGTCTGCTCCGTTCACTAATCGCGGTCTCAGCAGCGTCTCG  
ACAGCCACCAACCGAGTGAGACAGATGNCACACAGGACCGCAGCGATGCGATCACCCTACCCGCTCC

.....:Rv49T7.seq:.....  
CAGGCATGCAAGCTTTCAGTTGCTGAGTAATGTCCGCCAACGTCACCAAAATCGCGATGAATCAATCATGCCGCC  
AGGGCGGCCAACCAATGGTGGCGCGAGCGGCGAGCTCGATCGACGCGCGGAGGTTGCCGGCGCGCAAGTGAATCAG  
AACAGGTTGAGTCAATAGCGGGCGAGGATAGTGACGAAGGCAAGACCTAGATCTGCCGTGGAAGAAGAATCGAGTAT  
CCGTCGACACACCGGAAGCGAAAGTGTCCGCGATGTTGATGAGCGTCCGCGTGTGGCGCGGTGGCGGCGGTAGC  
ACCGTCCGACATACCGCGGGAACCGCGGCATCCGAATTTGGGGCAGGTTGTTCAAGGCGGTCGCACTACCATGA  
ATCT

## Clone Rv4

.....Rv4SP6.seq.....  
CCGGCTCGTATGTTGTGTGGAAATTGTGACCGGATAACAATTTACACAGGAAACAGCTATGACCATTAGCCCAAG  
CTATTTAGGTGACACTATAGAACTCAAGCTTGGCCGACGGGCGAGTCGATTGGTCGGGTCGCTCGACAGTTAG  
CTTATGCAATGCTAACTTCGGGGCAAAGTTCAGCGGATCGGCCGATGCCGGGCGTAGGTGAAGGAGACAGCGGAGGC  
GTGGAGCGTGATGACATTGGCATGGTGCCCGCTTCCCCGTCGCGTCTCGGGTAAATGGCAAGGTAGACGCTGACGTC  
TCGGTTCGATTGCCACATGCTGCGCTGCCCTGGGCATCGCGGTTTACGAGCGTAAACGTCCGCGGACCTGGCTGCC  
GCCGCTCTGTTTTCGCCGCGCTGACCCGCTCGCCCATGACAGTGCAGACCTGNACCGGGCTGGCC

## .....Rv4T7.seq.....

GTGTGCTGCAATTCAGAGCTGAGCCTGATGCACTCAACTTACTGAGCATGCTAACGCTGGTCGTGGGGCTCTTGTC  
CCGCGGTGTCGCGACGGGCACACGCTCGGGGCGTAGCTGGGAGAGGCCCGGTCAGGCCGGAGAGCAGTGCTCAGTCCG  
CCAGCTTGACCGACTTTCGATGAGAACGCGCTTCTCGCGCTATTGAACGGCGTGTGACGGTCGCTGAGCAGCGCTC  
GCCGAGTGGCGGCGCTGATTCTTTTCATCGAGCCAGGAGCGGCATTCTGTGTTCCGGCGCCTGGGGCTCGGCCCATCGT  
CGACGCGATCCGTCAACCACTCCTCGATCAGGTCTGCCCTCATGAAACGGGCCAACGGTGTCTCGGAGTAAGTGTGCG  
TGGGCACGCGAGCCGGGTGCTGTGGTACACCCACCGCTGCATGAACAA

## Clone Rv50

.....Rv50SP6.seq.....  
ATACTCAAGCTTACCAAGCGCGCGGGGCGCGGCGCAAAGCCAGGCAGCCGCGCTCGGGCGCTCGGGGCTTCCGC  
CGGCTCGGCCGACAGTTTCATCTTGATCGCGGGGCTCTCCGGGCGCGCTCGCGGACCTCAGCGGGCGCGGCTT  
CGCGCGAACCAATTCCCTAGCCATAGATAACCGCACTCAATGCACGGTTTGGCGGCAACCCGG

## .....Rv50T7.seq.....

AGCTTCCGTCAGCAGCCGCCCTCGCGGTCGCCGGGCCATCGGTATCGGATCTCATGACGAGCTCACGTAGGCCCGC  
TAGCCCGAGCGGGGCGCGGTCAACTGGCGAGCGCGGCGGACGCTGACTGAGCTGGCCGAGCTGGACCGGTTCAACGCG  
GAATACCGTTCTCGCTCGACGACTTTTCAGCAGCGGGCTTGCAGCGCGCTGGAAACGCGGCCACGGTGTGCTGTGTG  
CGCCGCGACCGGCGCTGGCAAGACGGTGTGCTG

## Clone Rv51

.....Rv51SP6.seq.....  
ATACTCAAGCTTGGCGGGACGCGGAACAGAACCGCGGTTCTTACCGCGGTGTGCGGGCGCGCATCGGCTCC  
CGACTAACCGAACCGGATGTGGGCTCC

## .....Rv51T7.seq.....

ACGTTGGCTCTGCGGGAACGTAATTCAGCGGCACGATTCGGCGTGGGTGCCGGGCGCGAGTTGCGTCGCTGGGAT  
CACCGAGCAGTCCGCGCGGCTGCCCTCGGGCTATGAATTGCACCGAGCGGAAATTCNCAC

## Clone Rv52

## .....Rv52SP6.seq.....

ATACTCAAGCTTGTGCTGTAATTCGTGGCACTGTGAGCATATGCGCGCTCTCTCATCGTGCCTCGGCATCGTCG  
CCGCGGTCATGGCGTCACTTACCCAGCCGAAACGCGAAACGAGAACGTGTTCCATTATAGGGTGTGAGCACCAAT  
ACCAGATTGCTACACAGGAATCAGCGAGCACGGGACGGATGTACGCCACCAACCCCATCTGGGTTGTAGCGGGGA

## .....Rv52T7.seq.....

CGTTGGTAGCCGATGCTGATAGTATCTTACTGAACATGATTTCCATTATGAGGCCCGGGGTGCCGCGAGCGGAA  
CGGTGCGCGCTCAGACGCGGGCGGCACTGACCAGGGTGTGCGGGCGAACATCGGCCCGGCTCGGATTCGGTCCGG  
GTACGGGGGACCAACCGCTTCGAGGTA

## Clone Rv53

## .....Rv53SP6.seq.....

ATACTCAAGCTTGGCCAACTCTCATCGGACTTGAAGGTGCCGTCTCGTTGGCGGCCCTGCTCCACGGCAGTTGAT  
GTACACAGGAATGTGTCCGGGCGCTGGCTTTGTTCTTGGCGGAGGTGCGCGGGGCGCATGATCTTCCCGGAAACTC  
GTCGGGAGAGCGCAGTGCATGAGGTTCTTGACGTTGATGGCGCGCAGGACCTCGTCGCGGAATGCCCGAATCGTGTT  
ATCCGGCGGGAGCGGCTGTATGAGGTACCGGCGGCTGACCGGGTGCCTGGACAGCGGGCGTCCGTCCAGCTCCCA  
CTTCTTGGCGGCGCGTCCAACNACTTGACTTCTCTCGG

## .....Rv53T7.seq.....



Clone Rv54

```

:::Rv54SP6.seq:::

```

ATACTCAAGCTTGTCCGGGTAACCCGCGAGCAGGGCGGTGGTGGCGGTGTCAAAAACAACACACTTCTTTGCGGTTCTC  
GGTGATCTTCAGACCGGCGCGAGCCAGCAACCATCGCCGCGTAAATCGGGCATCGCCGCGTGGGATCTCGCCTGGGT  
CGCCGATCCAGCGAATCGCGACGCCAGCAATGGGCGAGCGTTGCGAGCATAGTCGCGGCGCGCGGCGACACAGTGA  
CGGCAACGGTGAATCGCTGGCGGCGAACCGCGGTGAACAACGGCGGGCATCTCTGCCGCGCAGCGACCGCAGGC  
AGGGGTGCCCTGGGCGCAGCATCCGACGCCGAGACGACGAGGACCAGGCCAGTCAGTAGGCAAGACCGCTTGTCCGA  
GACATGAATCCACGACCT

```

:::Rv54T7.seq:::

```

AGCTTATTGAACCGGGGTGCAAGGCAAGTGGACCTCTAAGACTCGGGTCAGCGACCGGCGCAACACGAACGGC  
CGGACGACGCTGGGCGACAGGTCGCGGCGCTCCCCATAACACGACGACTCGTTGCTCGAGCGACAGGCTCGCGTGGCGGG  
TTGGGCGCGCTGCTGCTCCAGAGCTCGGCTCGGGTGGCGGACGACGCTGTTTCTCCATATCGGCCCCTAATCT  
CGAGGCGACGCCGTACCCGACGGCACTCCCAAAATGCAATCCGCAAAATGCAATGGCTCGAGTATTTCCTACAC  
GCAACGCTAGTTGGCGGATCCGTAATCCCTTTGGGCGCGGAATCCGAGCGAAATTTGTTCTCCGCTCCGCAATCATGCTT  
GTGATCTTTGGAAATTCATCCTCATATGCTCGATCGCTCATAGGGTCGACGGCAACCGGGCA

Clone Rv55

```

:::Rv55SP6.seq:::

```

CTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCC  
AAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGGCCACCTCGCGGTGTGTGGTGGAAACCATCTGAGCAGTGTG  
CCAAACCGGGGCGAGACGCTCCCAATTGACGTGAGCCCGCTCACTTGCTGGGTAAAGCGTCG

```

:::Rv55T7.seq:::

```

TAGCGCCCCCTCCCGGGCGAGCTCAGCGGGCTGGATCAAGGTACGCGCGGGATGTTGGCGCAATGGCAGGTTTGTGC  
CCGGCTTGATGTCCGGCTGTAGCGCGAGTATCCACACATCCCTTCGGAAGTCGGTGTGGGTGAATGATGTAGCGCT  
CTCCCTCGATCAGAACTAGTGGAAGCAACGCAATCCGTGCGGTACGGTTCGGGTCTGTA CTGATGTGCGCGACCTTGGCGT  
TGACACACTCTTTGGTCATTGCGCGCAAGTCGATCATCCGTAAGACGCGCGCTTATGACCCGCGCTTTGTGCGCGGTGG  
TAATCCGCGCATTCGGGTTCGGTCCGACCGGACGCTGACAGCGGCGCAACAGCGATTCTCCGGGTGTACCGCGGTGA  
TCTCGCGCAATACAGATACGCTGGCGCGCGACGACGACCAAGCCTGTGGGCTGTGTTCTGCAATATGCATGCTAATCA  
GGTCTTTCTC

Clone Rv56

.....Rv56SP6.seq.....

TGAACATATATAATACTACGAGCTTGCACAAAGAGACCTCGTCGACCAAGCAGGACGCGACCGTCGAGGTGGCGATCCG  
GCTGTGGCGTCGACCCGCTGAGGCAACACCAAGTGGTTCGCGGCACGCTCAACCTGCCACCGGCACCTGGTAAGACGT  
CCGCGCTCGCGGTCTTTCGGGTTGGTGAAGAAGCGGATGTCGCCGTGCGCGGGGGCGATGTTGTCCGAGATGACGA  
TCTGATCGAAAGGATTCAGGGCGGCTGGCTGGAATTGATGCCCGGATCGCGACACCGGATCAGATGGCCAAAGTCGG  
TCGCATCGCTCGGGTGTGGGTGTCGCGGGCTCGGCTCGCCCAACCGCGAAACCGGCACCTGACCCGCGAGCTCGCCAA  
GGCGCTCGCGGACATCAAGGGCGCGAAGATCACTTCGGGTTGACAGCAGGCGCAACTGCATCTTC

.....Rv56T7.seq:.....

GCTGAGCTCCACGGCGTGATCAAGGTACCGGCGGGATGTTGCGCAATGGCAGGTGTTGCCCGGGTGTGATGTCGGC  
GTTAGCGCGCGATTACCAACATCCCCGTGCGAAGTCGTTGGTGCAGATGATGTAAGCGCTCTCCCCATCGAGATA  
GTGAGCAGCAGCATCATCGTCGGGTACGGTTGGGTGCTACTGATGTCGGGACCTTGGCGTTGACACATCTTTGTG  
ATTGCGGCGAAAGTCGATCATCCGGTAAGCGCGCTTACGACCGCGCTTTGTGCGGGTGGTAATCCGGCATCGGCG  
TTGGCTGTCACCGACGCGCTGACGCGGGCGCACAGCGACTCTTCGCGGGTTGACCGGGTGATCTCGGCGAAATCAGA  
TAGCGTGGCGCGCGACGACAGCGCTGCTGGGCTGTACTTGCGAATGCGATCTGAATCAGGTCCTTTCTCT

## Clone Rv57

.....Rv57SP6.seq.....  
ATACTCAAGCTTGTGGTGACCTCGCCGGCGAACAGTTCTCGCACGATTTCGGGATTAGCGGGACTGGTCACCAAGTTG  
GGTATCGCGGAAGGCGCTGACGTTTCGCGCGATTAGCTGTTTATGGACGCGCGGCTGATGTCTGTATCAGCGAACTG  
GCTGTAATAGCCAGGGTCGCCACGCTTCATCCGGGCGCGACCGCG

## .....Rv57T7.seq.....

GATGATCGCCGGTGCCACCCCGATCCGTGCCTCGGTGAGCGGAACTGCTTCCGGTCCGCGACCACTATGTCGA  
CGCACCGACAGCGCGAACCCGCGGCCGCACATGCCGTTGATGCGCGCGACACCGGACGCGGACTCGACGAT  
GGCGCGCAACAGCGCCCTATTTCGCGCGCCGCGCCACCGCCATCCGGTACGGATACCAACCACTCCGCGCGCTC  
GCTGAGGTC

## Clone Rv58

.....Rv58SP6.seq.....  
ATACTCAAGCTTGGCGCAATCGAAACCACTGTTGTGCGCAAGAAATTACCGCGTGCCCGCGCGGATCAAGAA  
ACGCCCGCGCGCGCGGCTGTGCTCGTATGGCATGACGGGACCAATGTGCACGCGATTGTGAGCAGGCAACCGGTG  
CCAGCCCGCAATCCGGTGACACGGCGACACCCGCGCAACCCGCTATCGACGGCGCTGCTGTTTCGCGCTGTG  
GCCAGCTCGACGAGCGCTGCGGCAACCCGCGCGGCTGGCGATTGGGTCT

## .....Rv58T7.seq.....

TGCGCGGTTGGCCACANANCCCGCGGTGACGGCGACGATGCTGGGCTGGTTGCGGCCCTCGGCCACCGCGGCTG  
CATGCTGGTTGGCTGTCTTGGGACGATCCGAAATAGTCCAGCGGATCTGGTATTTCGCGGCTACCCGCGATTAC  
CCGCGCGGCTCGACGAGTTTTCGCGCTGGACTACCGCGTGCCCAATCTGCTGAATCGCGCGGCTGGTGGCTGG  
AATGTCANCGCGTTTACCTACGTGACCTTGATGGGATCCGCGGGNT

## Clone Rv59

.....Rv59SP6.seq.....  
NCGTGGACACCGGTGTCGANCGCCACGCGCATGTCTGCANGTCNATTCGCTCCTCGGCAACATCTTGAATGCCGA  
GCAGCGCTGGGCGTGATCGCGCAACCGGGATGACCGCTCGCGGATCCGCTGCACATCCCGCGCGACGTGACATGC  
CGCGGGAAGGCTCGACGAGCTGGAATCTCAGCGACGAGATCCGGAATTGATACCAAGCAGCGTCTACTCATGGAAC  
CTCGCGCTGAATCCCGTATGGCCACGGTGTGACTATTGTCGACAGTCACCCGAGATAGTCTTACGGGTCGCT

## .....Rv59T7.seq.....

CATGTATTGCGGTGCTCAGGCGCCACGCTCGATGGTTTCTCGAAGTCTCCGGGCTGGTGTACAGCTTCTCGTTGATC  
TCGTTTCGCGACCGCTCTCTTCCGCGCAGCAGCCGATCTCGATCTCCANAATGATCTTGGCGCGCGCGCGCTT  
GAGCAGCTCTGGGCGATGGCGAGTTCTCATCGATGGGCACTGCCGACCGTCCCATGATGCGACGGAACAAAGATG  
TCACCTTGCTCAGCGGTGCCNAGATTCANAAAGGCGCGACATCTGTCTACTTGTCTTGGGCGTGGTCCGTGTC  
AGCCACAGTGACGGGTACTTGGCGCGATAACGTGGT

## Clone Rv5

.....Rv5SP6.seq.....  
GCCACACGACCCCGCGCTAACTGTCTCAGGAAATGCGGCCAGGCGCGGTAGCACGTGGTATCCGCCATAAAGG  
TGACCTTAAGCACCGCGCTCCCAATTCTCGAACGACATCTTGTGGAAGGTGCGGTGCGCGCAAGATCCCGGCGTTGCTC  
ACCAACCGGTGACACGCGCGCAATTCGTCAAGCGCGGTCTTGATGATGTTTCGCTGCGCGCTCTCGGTGGCGACGCTG  
TCCTTAGTTGGGCAACCGCCCGCCCTTGTGCGGAATCTCGCGACGACCTCATCGGCCATCGCGCAAGCGCGCC  
GTGCGGCTCGCGGGCGCCACCGAGGTGCTTGACACGA

## .....Rv5T7.seq.....

CAGGATGCAACCTTTGTCCACAGCGGCTCTACTCCGTGCAAGGTCGACCGCTTCCACGTCGCCCGGTGACGGTGT  
CCATCTCCCTCAGCAACCGGTGAAGTGTTCGATCCGCGGCTTCAGG

## Clone Rv60

.....Rv60SP6.seq.....  
TTTGAGACGCAACACGCGCAACAGCAGATTGCGGTAGCGCGGACGCTGCTCGATTGATCAGCTCGCGCTCGCA  
GTCAGCATGGCCGCGACGCTACACGATCGCCGTGCTCGATGACACGACGAGCGGTACGCGCGCCGTAAGCGCGCC  
AGGATTTCGGCGAAACGCTCTACGTGGCGGGTGTACTGGGTGTCGAATGATTCTGGGGTGCATATCGCTCCTGCAAT  
GCTCGACATAGATCCGTGCGCGCATCGCTCGACAATCCGGGTGAGTGGAAATACATTCGCGATACGCGACGTGCG

CGGATCGATGCCGACCAGAAATACGACCACATGGCTCTTGTGTGNCAGTGTGTGGCGCATCAAATACCCTCAGTGCCGCT  
CCGAC

::::::::::Rv60T7.seq::::::::::

TTNCCGCGCTTNAACGCTACTTCNAGACGATGCTCGACGCGTGTGAGCACACGGCGCTGCTGTAGACGGCAGCGGCGCAG  
CTGGATCGCGCTTGGTGACACCCAGCGCTCTACGCGCGTCCGTGCGTCTCATCGGGTACCGAACATATTCCGGTCTGTT  
GCGCAGAGTGTGCATGTGCGGGCTCTTGTGAACGAACATAGCAAACGCTATATGTCTGTGGCGGCTCTGCAGATATCGC  
GATAATACGTATATACATAAGGTGGCGCGCATCTATCGGTATATCCGTTATGGCGGACGTGCGTGAGCGTGAGTCTGC  
GGCGCATCGCGCACTTCGCGATCGCGTGAATGCTCTCCGCAATGCGCGCATGCGTAGC

Clone Rv61

::::::::::Rv61SP6.seq::::::::::

GGTGATGACGCCTTGCCTCGAATGAGTCATTGACTACTCCCGTGGTTGTCTCGGATGGTGGAGTGCCGCGCAGCGCT  
TGCCCGANGTCGCATCGCGTCGCGGGCTTCGGGGAGCAGACTGACCTCGCAGATGGAAGTCTGTGCCATGCCCGCGA  
ACGGCGAGCTCGATGCTTGTTCGAAGNGCGCANGCGGTTTCGATCTTGTCCGCGTCAACGCAGATCGGATCTCGCC  
CGGGTCTGCATGACGATGGCGCAGGCCCGCTCATGTCCCGTAGACGGGGAGATACGGGACGCCGGATCGAGACCT  
ACGTAGCGCGGGCGCCATCTGTCCATCGCGAAGAAATGACGGATCGCGCAGCGCGCTCGCGTCGCTTCGATGTCAACG  
CAGATCGCCACGCGAGATCAGCGATGCGCGGGC

::::::::::Rv61T7.seq::::::::::

CGGTACGCGCGCAACAAACGCTTGTGACGAGCGCGTCCGAGCGGTATCGGCGCTCCACCGTATGCACAGCTCCTTC  
TCCAGGTCTACGCCGACGCTCGCGGTCCACATTGGTGAGCTTGGCGAATGCCCTCGGCAACCTCGTCGAAATCGCGCTCC  
CGCTCCGATCGAAGGTGCGCATGTCAAAGATCAACTCGACGTAGTAGCTAGTTACCGCATCAGGTCAGTGTCTGCTG  
GCTTCGAGTCCGCGCGAACAATGGCCATTTCGCGGACTCTAGAATCCAGTCATGCTCTCGGTGACGACGCTTGGC  
GATCACATAGCTCGACCGGATCGGAGAGAACTCTGTTCTCTCT

Clone Rv62

::::::::::Rv62SP6.seq::::::::::

ATACTCAAGCTTAAGCGCAGCATACCGCGGCTGCTGGGCATCCGACAAACGGGGAGCTCAACGAACGATTCCTG  
AACGAAGGGTCGTCCACCACTCCAAACCGAAGGTTGCCAGCCCGGC

::::::::::Rv62T7.seq::::::::::

GCAAGTCCGCTCAATGTGGTTGTGATCAGACTACGTCGCCTCAATCAGCTCAACAGTCAACCCGTGGCGTGCTGC  
GCAGATCAAGAGTCTGGCGCCGCGCAGATGTGGGCGAAGCAACAGGTAATAACTGGTCGCATGGGTCAACCTCATTTG  
GGCGTTGGCGATCGGGTGACAGCCCGGAGTGGCGGTGCAACTCAACACCGCCTTACCGATCTTTTCTGTGAAAAATG  
GCGGTCTGTGTGGGGTATACGTCGCGATCCACGAGGCGGAATCCGCTGAGCGCACTGA

Clone Rv63

::::::::::Rv63SP6.seq::::::::::

ATACTCAAGCTTCGCGCCCTCAAGCGGCTGAAGTGGTTCCGCGCTNCCAAACNGTCGGGCAACTCGCCGATGGGCGATG  
GTGCTCGACNCCGTCGCGTATCCCGCGGAGCTGCGCCGATGGTGACGCTCGACGGCGCGGTTTCGCGNCGTCC  
GACTTTGAACGACCTGTACCGCAGGGTGATCAACCGCNACNNNNGNTGAAAGGCTGATCGATCTGGGTGCGCGGAA  
ATCATCTCTCAACAAACNAGANICGGATGCTGCNNGAATCCGTGACGCGCTGTTTCGACAAATGGCCGCCGCGCGCGCC  
GTCACCGGGCGCGGCAACCGTCCGCTCAAGTCGCTTCCGATCTGCTCA

::::::::::Rv63T7.seq::::::::::

TGCGCATGGCAGTGTGTGCCGGCTTGAGTCGCGTTAGCGCGGATTCACACACATCCCTTGCAGAGTCGTGGGTGCAAT  
GATGTAGCGCTTCTCCCATCGAGATGTGGAGCAACGCAATCCGTGCGTACGTTGGTCTGCTACTCGAGTGGCGCANCTT  
GGCGGTTGACACCATCTTTGTATTGGCGCGAAGTCGATCATCCGGTAAGCGCGCTTATCGACGCGCGCTCTGTGCGCG  
GTGGTAATTCGGGCATCGGCTTGGCTTCAACCGGACGTGACGAGGCGCACACCGATCTTCCGGGTGACGGGTGATC  
TCGGCGATCAGAACCTTGGCGCGGACACAGCGCTGTGGCTGTACTTGC

Clone Rv64

::::::::::Rv64SP6.seq::::::::::

TGGGTGATCAGATACTGGCTAGTTGGTCGGGTGGGTGATCGAAGATCGCGGTGGCGGCGACGTTACTCGCGGTGACG  
CTGTTAAGCGGTTACTGATCTCCACGGCATCAANGAATTANATCCCGAATCGGCAACCTGGGACAGCGTCGAGTCCG  
CAGCGCGCTCGCGCCCGCCGCTCGCGCATGCTCACATACCACTCGATCGCTCGGGAGATTGCTGCTGCGCGAC  
CGACCGGCGACCGGGCGGCAACCGGAGGACCAAGATTACGACACCACTCGTAGCCGATCTGGCGCGCGTGG

TCGTAGCGGTTGCGACCANTCCGCGGACAGCTCCGCCACGCGACGGGTGGGATACCCGCGGTCAAAACACACGAGCGGCGAGAGATCTCTGGCGCAGCTGACGCGGACGCGGCGGGTATGGCCAGTCCCGACGCGGCTTCACCTGGCCATACCGCGTGGATGTGTTTGCCGCACAGGAATCCCATCTCAATTATGACCTGTTGTGGGCGAGCGGGTATCGTACGCCGCCACGAGGAATCGTCATGCTATCTCAGCTCACCAGAGGCGCTCTCCAGCACACCGCATCCGAGCTGCACACNGTCGCACATGCTCTCGGCGGATCCGCTCGCAGACAGACGCCANTGCTCGGATGCTGTGCGACACGGGTCCGAGATCACCGCTCGCACGCGGAGATCGGCACACGCGCAGCGCATCGATCATATCTCTGATCGGCTCTCCACCACCGAACAG

ATATCTCAAGCTTCGCTGAGCGGGTGGGGCAGCATCACTCACCGCAGCTGCTCGGTGGGCGTGGATGCCGCCGGAT  
CAACCACCACTCACTTCTCTCTGGGCCCGCTGGCTCGGAAAGACGTCTGCAGCGCGTATCTCGTGGCNCAGCGCTTGA  
TCTTCGCGAGGGCCCTACCGCCAAACCGTCGGGGGTCTTGGAAATCTTCGGTGTTCGTCGCCCAAGCGCCCGCGAG  
CATCGACTGCTGTAGAGCTGGATCGCGCAGCCACGGCCGGCTGAGCAGACCCCGCAGCTCGGGAGCCGCCGCTTCTA  
TGC CGCGGTCCATCAGGCTACCGGCTATTATTCTGTCAAGCAGGCGCATATGTT

GCACCTCAGCTGTTACAAAGCCTTTCACAAATCTGAAATCTCTGACCCGATACCTTGAACTCTGCTTCCGCGATAAT  
CTGCTTCCGGCGTGGAGCGCGCGCAAACTACTTCGGCATCAACCGCTCCGCACTGGATGCGACCAAGCGCGCTC  
CTGTGGCGCGATCGGTGAATCAGCAGCAGCTACACCCGTACACCAACCCCGACGGCGCTGGCCGGCGGGAACGT  
GTTCTTCGACACCATGATCGAGAAAGCTCCCGGAGGCGGAGGCGCTGCGTCCGCCAAGCGCATTCGCTGGGGGT  
ACTCCGCGACCCCAATGATTTGGCGCGCGGCTCATCTGACGCGCGGGCAGCG

ATACTCAAGCTTGATATAAAGATCGGTGAGCGATTCAGTTTCGCTCGCGCGGGTTTCGCGCTCGGCGCGCGGATCGCG  
CGTACGCCCTCTATTGGTGATCAGATATCGGCTAGTTTCGGTCGGGTCGGGTGATCGAAGATCGCGGTGCGCTGCG  
CGGTACTCGCGTGACGCGCTTATGACGGCTGTAGTACTTCACGAGCATACGAAGATTAATCCGAATCCGAACTCGGCAACG  
CTGTCGCACCGCTCGAATCCGCGAGCGCGCTCGCGCCCGACACCGCTCGGCGATGTCATACATACCACTTCATTCGCTG  
CGGCGAATTCCTCGCTCGGCGACCGACGGCCAGCGGCGCGGCGGCAATCCCGCGAAGA

CCTCATCATATGCCGATAGCTCTACATATTACGAGGATACCAATGCTGCTGGGTCGGGATCGACCTCGGGGACAC  
 CAACTCCGCTCGTCTCGGTTCTGGAANAATGGCCACGNCGTCTCTCTGCCAATCTCGAGGCGCTCCAGGACACCCGTG  
 AATTGTCGCGTCTGCCCGGCAACGGTAGGTCGTGGTCNCGCAGCCCGGCAAGAACAGGCAGTGACCAACGTGATCGC  
 ACGCTGGCTCGCTCGCTCAAGCGACATGGGACAGCACTGGTCTACATAGAGATTGACCGCAAAATACACGCCCGGAGATCT  
 CGCCGCATCTCTGTGAATCACTGACGCGGACCCGAGGACTCTCGTGANGACATNACGACCGGCTTATCACACCCGCCCTNC  
 TTCAATGACCCCACTCTCNGGACCAAGGACCCGCGAATCGGGCTCACTTNGGCATGTCNACAAACCAACGCGNCGCC  
 TCGGCTACGGGCTCAACACGAGGACAGACAACTCCGCTCTCGATTGGTG

ATACTCAAGCTTATCGAGCGCGGCATACCGAAGCGTGGGAAATCCAGACCGAATACCGCGACGCTGCTGGACACTTTG  
CGCGCGGACGATGTCGGAAGAAGGACAGCTTCGACCGACCGAGCTGCGGAAGCAATCTTCTGACGTCGAAAACGGCGCG  
CGGCTCACCATGTTCTGACAACTTCGGTGGCGGATCCGCTCGGCAAAACCGCCATCAAGACACCGCGGACGCTCGG  
ATCGAAGCGCGCAACCTTGCCCCAGCGCGTCCCGAGCGCGGCTTCAAGCGCGGATTCGCATGCTACCCAAAGCG  
CGTGAAGGCGCGCGGTCCAGCGGCCAACCGCGGACCGGCGCAACGGTTGCGCGCGCGCACCAACCGCTCCGTGA  
CCGCTAGTACGCTGCCCGGCTGACTACTGCTGCCCGCGCGGCT

TGGCCGGGGCTGGTAGCCCGCGTATGGCAAGGTTCCGCTCAATGTGGTTGTGATGCAGCAGGACTACGTTGC CCTCAAT  
CAGCTCAAACGCTACCCCCCTGGGCTGTGCGCAGCATGAAGGTCGGCGCCGACGATGTGGCGAAGGCACCAAGGTT  
AAGAAGCTGGTCGCGATGGGTGCAGCCCTCATTTGGCCGCTTGGGATCCGGTTCGACGCCGCGGATGGGCTCGCTGCAA  
CTCAACACCGCCTTCACCGATCTTTTCGTGAAAAATGGCGTCGTGTCGGGGGTATACGTTCCGGATTCCACGAGGGCG  
GAATTCGCTGAGCGCGAGCTGATCCGGGCTCGCCGCGCGTGATCTTGCCCTGTGTGGTGTTCGAGCATACGAGCAG  
GTTCGAT

## Clone Rv68

.....:Rv68SP6.seq:.....  
GTCCAGTCAAGCATCGGTCTCTCCGACTACGCCAAGANTGGCGACGTGTCTAGTGCANACAGCGGANATGGTGGCGCC  
TATGGTCTGACCGTCAACAAACNGCGGTGANCGCCGTTCTGGTCTGTGCACCATCGAGCCGTGCCAGCCCGGCGCGTGC  
GTCAAGCCGATCACTGGATGCTCTCTCGNGTTTCAATCANGTACANGCGACGTTCCGCCACCATCGTGGCGGGGCAC  
GGTTAGCGAGAAACCGCGGCACTTCAACGATTGCTCGGTGATGCCGTGCAACAGATCGGGCCTATTGTCCAGAGCCAG  
TGTGATNGTATTGGCCCGGTGCTCCTCGTCGCAACGATGCAACACAGATCCGTGGNGGACGATAGCGGCTGACAA  
NTGGGGGCAACACATACATGCCATTTCTTCATTTACGCCCAACACCCAGACTTCGTCTCGATGNGCCG

## .....:Rv68T7.seq:.....

CACGCGGTCTGGCCGATCCGAAGATCCCTTTGCCGGCGTGGCGGCTCTGCTCGGCGGTGTTGTACACTTCTCGAAACA  
CTTCGGCACCGCAACACCACCGCTNGCTTGAACACCGCCAACATCGGCAGCAGATCTTGATGGTCTCGGTGAATCCCA  
CGGTGACTTTGGAGTGGAAAGCGCCATCTGATCGCCGCGCCAGACATGAGCTAGCGGAGGAAACAGCAGCGCCG  
TCACCTTGGCGAGCAGCGTCTNGGTGATATGCTGGCGGCTTAATCTCTGTGAACAGTTGGATTGGGTCAACTGGCAG  
CCTTGGGTCTCCGGTGGTGGCGANGTGTANATAAGCTCCCGGGTCCGTCAACGTANTGGCAGGCGGCGGTACTCGG  
CGGGTCAACGAGCCCGCTCGTGAACATCAGCCTTTGGACCGAAGGGGATTACATCTCCGACGGCGGCCCTCCGAAA  
TCGGACATGTCCTTTGATCGTTCGCAACAN

## Clone Rv69

.....:Rv69T7D3.seq:.....  
GGCCATGTCAATCGGTGGTACAGGTAACCGCGCGGTGTGCGCGGTCTCGGAGATCAGAAGCTGGTCCGAGTTGAAC  
CGCGGGCTTTCAAGCATCGCGATATCGCGGAAAGTCCGGCGCTTGGCGCCCACTAGCGCGCATCGCCACCTAGCA  
CACCGATGGCGAAGGCCATGNTCCGGCCACCGCGCGCGGTGCATCACCAGTTCATCGACTAGGAAGCTAAGCGACA  
NCTTTGCGAGGTGTTCGGGAGTAGCTGCTCGGAAATCGGCTGGAAACCGCATCAATGGTTCGTTCCAATCGAACCG  
GTTACCCGATCGTCAAAAAATCTCCGTCCT

## Clone Rv6

.....:Rv6SP6.seq:.....  
GGGTCTACAACCAACCGGCTCGACTTCTGGGCTTCCACCGCTCGCGCCGTGCGGACAAACAGCGCGGTGCAACCGACA  
CTCGTTGTGATGTCCAGCTATCACTCCGGTAGGCAACCAATGACCCCTACCGGCTATCTACCCCCGATCTCCAG  
GCTCCGCGGATCCATGCGCATCCCGGTCCGGATCCC

## .....:Rv6T7.seq:.....

CAGGCATGCAAGCTTGTGATTCCTGGCACTGTTCAGACATATGCGCGCTCCTCCTCATCGTGCCTCGGCATCG  
TCGCGCGGCGGTGATGGCGTCAACCTACCCAAGCGGAAGCGGAAACGAGAACGTGTTCCATTATTAGGGTGTGAGCAGC  
AATACGAGATTGCTCAGCAGGAATCTACGCAGCACCGGAGCGGATGTCAAGCACCAACCGCCATCGGGGTGGTAGCCG  
GGAAATACGGCTAACGCGGCTCCGGTGCAGCGAGCCAGCGCAGACCTCGCGGCGGACACGGCTAACACGACGACG  
CCATAGTTGTTCTTTCGGGATGCGCGTGTGTTGCTGACATATCGGCGCGCGCGCGCGCGCGCG

## Clone Rv70

.....:Rv70SP6D2.seq:.....  
NCTACGCTGCTGAATGTTGTGCGCGGAGGANTCAAGACCCACGCGGTTGTACGCGGACNTGCGACATGTTCAACCG  
CCGA

## .....:Rv70T7D3.seq:.....

CTAACCAACAGCATGGTGGTTGGCGCGTTCGAGAGGTGCGCGGTGCGCACAAACGGGAAGATCGCCTTGAGCGTCG  
TCGACCGCGCTCGTTCAGTTCGGTCAACGAAGTACTGATGCCGATCATGTCCGCTCGCATCAGCGTGCAG  
CGGCGACCCCTCGACGAGCTCGGTGCGCGCGCGGCCAGGGCAGCAGCTGTTTTCGCGCATTTGTCTCGCGCGGTAT  
AAGGGANGTCGGTGCCTCCGCTGCTGTGGTTGCGGAATAACATCTTCCCTTCTGCAACAGGATGAGAATGGTTTTA  
ATTGCT

## Clone Rv71

.....:Rv71SP6.seq:.....  
CTAAGCTTTCGGGTCCGCGCCACTAGTACCGCGTTGCCGCCCCCGCCAGCTAGAATGTTCCGCCCATTCGCCGTTTC  
CTCCGCGCGCGGGT

.....Rv71T7.seq.....  
TCTGGTGC CGGGTGTGCCGACGGGTCCGTCCGCCTCTGCTTCAGTGATTCTGTGATGCGACCGGCAACGTCCTCGTTG  
TTCGGTGTCTATGTGTCCGTCTCTCCTTGTGCCGATACGATT

## Clone Rv72

.....Rv72SP6D2.seq.....  
GCGATCGNTNACCACAAGGGCGCAACCGTTCCGCGCTCGCATGAACGTGCTGCCGCTGGAGAACTGGCGTCTGCTGCC  
ACCTGCTCGCGGCATCGGCACCTTCGAGGACTGGATTTCGACGCGTGGCCGACCTGANGTGGCGGTGGACNNGTGTG  
CACCCGGTTGATTCTCGGCCTTGCCGGGATGCCACCTGCGCCTGGTGGTCGAT

.....Rv72T7D3.seq.....  
CGTGACCGGACGGGGTCCCGCGCAACCGTCTTGCCCAATTGCCGGGACTGGGGCTGGAGTATAAGCGGGCCTGT  
TGCCGGAAGATAAAGTCAAGCGGTGACCGAGCTGAATCAACATCGCCGCTGGCGATGTCGCGTGACGGTATTAAACG  
ACCGCCAGCGATGAAAGCTGCCCCATCGGGATTGCAATGGGTAGCGGCACAGACTGGCGCTGGAAACCGCCGACGCA  
CATTAAACCATACCACTGCGCGGTGGTGCAATGATTGAACGTGCACGNCCTACTACGCCAATATCCGCCAGAAC  
TCACTATTGCGCTGGG

## Clone Rv73

.....Rv73SP6.seq.....  
ATACTCAAGCTTCTTACCCANAGCATGAACCCCGCGTCCAATGCCGCCACCGGTGCTGTGCGCCGGCCGGGTGCG  
GGCACAATCGCCGAGTTCCGCGAACAGATCCTCGAAGGTCTTACGCGCCAGCGATTGTTGCACTGTTCAGCCAGCCAA  
TTCAGCGTGGTTGACGCCACGCTTCCGCAACCGCGCGCGCGCATTAGGGCATCCTAATATAGGTTAGGCTACCCCT  
ANTTATTCCTGTGGGTCAAAGGAGGCGAGCGGACCTGCCGATGCTGTTGCGAGTTCCGCGCGGAAGTGCCTCA  
GCATGGCTGTCCACCGCATGGGCCCCGGTCCGCTGCTGGCCCGCGCCAGGGCGTGGCACGCGCTGGCCCGCAATAC  
ACCGAATTGCAACGGAATCGCAAGCGGTGCTCGCTGCGGTGCGAGCAACTCTGGCAGGGGCCCGAGCGCCAGCGTT  
GCTCNTCCCATCAACCGTTCCGTATTGGCTAACCACTGCACGGTGGCACCGCACACCGCCGCCACAACCGCGCCCC  
GGTATAC

.....Rv73T7.seq.....  
GGCCGAACCTTAATCGGTTGTGGCGGCTGCCGAGTTGGGTCACTCGGGGGGTGTGCACTGGCACATGGTGGGCGGGAT  
TAAACGCAACAAGCCGGGTGCTGGCTGCTGGCGCACACCGCTCACTCGGTGGACAGCTCGCGGTTGGTGACCGC  
GCTGGATCGGGCGGTTGTTGGCGGCTGGCCGAACACCGTCTGGGACGCGGCTGCGGGTTACGTCACGGTCAGCCT  
CGACGGTGACGGATCCCGGGCGGGCTGCAGACGACGACGCCCGGCGGTAGACCGGATTGCGCGCAGGTGCAGGA  
GTACAGGGGCTCGAATGTCGCGGTTGATGGGCATTCCGCCGCTGGATTGGGACCGCACGAAGCCTTTGACCGGCTG  
CAATCGGACACAAACCGGTCGTCGCGATGTTCCCGCACCGCATCGGTCTGTCGCGGGCATGTCCAACAACCTTGAAT  
CCCGTCAACATGGTCGAC

## Clone Rv74

.....Rv74SP6.seq.....  
GCTTCCCTCGATACCTGCACGCCCACTCGGGCCAATACGTGAATGTCTAGCATTTTTCACCGGTTACGGCGGTAG  
TCGAGTAGTACGATTTGATTAGCCTGAACGTACTCTCGACGGCCAGCTGACGAACGGGTTTGACGGA

.....Rv74T7D3.seq.....  
TCAGCTGTCTGTAGAAGGCTGGCGATACTGTGCACTGTCTGATATCGCNCNGTNGTGGGACTATNCAAGCCATNANG  
ATGCGGTTTCGNNNNNTGCAGAGNATCCTGGNACACATNCGGTTACGTTAATCANCATCGCGANTTNCNCGTNTTCG  
ATTATTTCTGCTAACGNNTCTNNNAGTGCTCGGGTGCAGCTTAGAG

## Clone Rv75

.....Rv75SP6D2.seq.....  
NCTCTGCCGCGCNAAGCGCAGACTCGGACGGCTTCGTCGATCGTGAAGCGACNCTGCGATGANAGATATCGNTNAC  
ACTGCTCANAAACTTCGGATCATCGNTGATACAGGCCAACGGGTAGCGGTTGCCAACCGCTTCGTCACAGANATG  
GGATCGTGACGANCTACGCTCGCAGGATATGTGCGNGACCCNGNTCTAGANAN

.....Rv75T7D3.seq.....  
CACTTCATGCTCGTGGTGGGNTCGATTGTCNCGAGNGGTTAGTCTCCTCGAGTNGTGACGTATCACTCCGGCNGAC  
TANCCGTATCNGGCTCCGCGACCGGCTCAACTGGTCTAGGCCACACCGGGGAGATNCGACCGCGGNGCTATCGACCNAT  
CACGGCTTGTGNCNNAAGATAGNCGCC

## Clone Rv76

.....:Rv76SP6.seq:.....  
ATACTCAAGCTTGCCAAACCGCCACCGTGATCCGGGGGGCGAGCACTGCTCGGCCGACCAAGTACGAACCAACCTGCGG  
TGCCCAAGGCCATTGACAATGTGTGTCGGCGCCCGCGAGTTCTAGCACAGCAACGCCCGGGCCACACAGGGGGCG

## .....:Rv76T7.seq:.....

CGGTGCGGTGTGCTTGCGGGCGTGGTATCAACACCGCCCAAGAAATGGGGCACAAGAAGGATTTCGTGGAGCGGTGGC  
TGTCGAAGATCACCCCTGCGCCAGACCTGCTACGGGGCACTTCTACATCGAGCACAACCGTGGCCATACGTCCTGGGTGT  
CCACACCGGAAGACCGCGGTGCGCGCGGTTGCGCAAACTTTGTGGGATTTCCCGCCCCC

## Clone Rv77

.....:Rv77SP6.seq:.....  
AATACTCAAGCTTCGCGGAGGTGGTGGGGCAGGAGCACTACCGCGCCGCTGTCGGTGGCGCTGGATGCCGGCCGGA  
TCAACACCGCTACCTGTCTCTGCGCGCGCTGGCTCGGGAAGACGTCGTCAGCGCGTATCTCGCGCGGTGCTTGA  
ACTGTGCGCGGGCCCTACCCCAACCGGTGCGGGGTCTCGGAATCCTGCGTTTCGTTGGCGCCCAACGCCCGCGCA  
GCATCGAGCTGGTAGAGCTGGATGCCGCCAGCCACGGCGCGTGGAGCAACCCCGAGCTGCGGGACCGCC

## .....:Rv77T7.seq:.....

GATGGCACTCAGCTGGACAAGACCTTACAAAAATCTGAAATCCTGACCGGATACTTGAACCTGGTCTCGTTCGGCAA  
TAACCTGTTCCGGCTGCAGGACCGCGCAACGTACTTCGGCATCAACGCGTCCGACCTGAAATTTGCAGCAAAACCG  
GCGCTGCTGGCGCGGCAATGTTGCAATCCGAACAAGCAGCTCAACCCGTACACCAACCCGGAAGGGCGCTGCCCCG  
GCGGAACCTTGTCTCTCA

## Clone Rv78

.....:Rv78SP6.seq:.....  
AGCACTATGACCATGATTACGCCAAGCTATTAGGTGACACTATAGAATACTCAAGCTTCTGGCGCTGCTGGTGC  
GGCTGCGCGGTGCAGGAATGGATTTTACTGCCATCTCTCGCGACCTGAGGTGGTCCAGGCTTACAAACCCGACCCA  
CTCGTGACACCGGACGGGTTCGGCGCGGATTTGGCGCGCGCTGCTGCAATGGGCGAGACCATGCCCGCGCGANCA  
CCGCGAATGATGCCCGCGCGCTGCTACTGTCTACGGCAGCGATGACCGGCTGATCCCATCGAAGCGAGCGCTGCGCTG  
GTCAATGNTNNGGATGCGCCAGCTGCANCTGAANGANTATCCCCGGCTGTNCCACNAGGTGTTCAACGAACCGGAN  
CGCAACCAAGTG

## .....:Rv78T7.seq:.....

CAAGGCATACGCCAAGACCAAGGGATCGCAGTCACCTCCGTCAACGGCCTGGTGGCGGGCACGGGTCCGTGCAAGGA  
GAGCTGGCTGGCCATGCAAAAGCGCGCGCGCTTATCAGGAAGCGCCCGGCTTGTGCGCTTTCTCGATCGACACATT  
TCCGAGGCTGTTGTGGTTGGCGCAGCTGCGCGGAGACCGCTGGGATGGCGATCGCATCGGAAATCGGATGGC  
AACACTGAATACGAGCGCATCTGCGCCAGCATGACTGTTTCGACTACGTCGTTGGCGAGCGGGANGTAGCGTT  
CACCAGCTGGCCTTGGCCCTGGCGAATGACTTCGCGTTGACGACTCCGCGGACTAACCCGCGTANTGAGCAAGGAC  
AGATTCTGCGCACACCTCTCTCGTGGTTCGACCTTGACA

## Clone Rv79

.....:Rv79SP6.seq:.....  
AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGCCGGTGATCTGGGTGGC  
CACTCGCGGGGACCATCTCATCACGACNGCAACAGCTCCGGCTTCGGCGACGACGATCGCGTCTGCGATNGTTTG  
TTCCGGCGCGCTCTCCGCGCGCTGCGCCGCGTACCGCGGAAGCCGCCAAGGTGTTGACNCTTTGCGGGGTGAAGCCGATGTGTG  
CATCACCGGATNCCCGCGCGGTGAGCANGCGATTGCTCGGCCACCGCTCACCGCCCTGCANCTTGACNGCATG  
TGCGCGCGCTCTTGAAGAAACCGGTGGCGGGGCAACCC

## .....:Rv79T7.seq:.....

CGTTGAGATCAAGCTGCGCACTGTGACGCGCTCGGTGGTGTGCTCGCGCTGCCGGGATAACTCGTTGAGCTTGCCCA  
GCGCGCTGCTCGCGCGGATCAGCCAGCAATTTCGCGCGCAGGACGCCGAGGAGACGGTGAAGCTCGCAAGAAACCTTA  
TGCGGACCGCATGATTACGACCGCGGATCAACACCTCTGGTCGAGCTCAAAATTTGCTTCTTAAACCGGCGATG  
ACGCGATGACGTCGAGCTGGTTAGGTCTCAACAGGTTACGAAACGATCTCGGAATTTGTCAAAGGGGAAGTTAAGA  
AAATGGATGATTTCATACCAATTTCTGCTGGACGATCGTACTTCTGCTATAGGGCTCAGGGGATCAGACGCAACG  
ACCTTACGCGACACCGGATCCGCGCTGCGCGCGGAACGGCACANGCGCAACCGAAGGGCCAAATCCGACATCGG

:::::::::::Rv02S2P6.seq::::::::::::  
 AACACGCTATGACCATGATTACGCCAAGCTATTTAGGTGACATATAGAATCTCAAGATCTGGTACCCATCCGTGATA  
 CATTTAGGCTGCTCTCCCTGGGGGTCTTACTCTTCACGAGCAAAACAGTATGCCCTTTCAGAGCCAGATCTTGAGCAAG  
 ATGAACCAAGCTGAGGTTGTGTAAACGCCACTTATTATGGGCAAGTACCCCGATCACCGGTTGGAAATATCTCTTCAGC  
 ACGTCCGAATCGGCTACCAACCATCAGCATATGATTTATGTTGTTCAATTGTATACCAACACAGTGTGCTCAACCG



TCTCTCGAATTTCATATCCGGGTGCGGTAGTCGCGCTGCTTTCTCGGCATCTCTGATAGCCTGAGAAGAAACCCCAAC  
TAAATCCGCTGCTTCACTATTCTTCAGCGCCGGGTATTTTCTCGCTTCCGGGCTGTATCATTAATACTGTGCA

## Clone Rv83

.....:Rv83SP6.seq.:.....  
AACAGCTATGACCATGATTACGCCAAGCTATTAGGTGACACTATAGAATACTCAAGCTTANCGCCACCTCCCGGGCG  
GAACCTCCAGCGCGTGGATNAAGGTACCGGCCGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGTTGANGTCCGCGTT  
AGCGCCGATTCCACACATCCCTTGCAGAAANTCCGTTGGGTNATGATGTNNCGCTTCTCCCNATCNANATAATG  
GANCAACGCNATCCGTGCGGTACGGTTCGGGTCTACTCCATGTNCGCGACCTTGGCGTTGANACCATCTTTGTCTATT  
GCGGCGAAAGTCNATCATCCGTNAGCNCGNTATGANCGCCGCTTTGTGCCGGGTGGTAATCCGGGCATGCGCNTT  
GCGTCCACCGCAAGCTGCAACGGGGGNCACACGANTTTCNCGGTTGAACCGGTNATCT

## .....:Rv83T7.seq.:.....

TGTGTGTGGTAAACCATCTGAGCAGTGTGCCAACCGGGGACGCGAGCTCCCAATTGACGTGAGCCGCTCACTT  
GCTGGGTAAAGCTGC

## Clone Rv84

.....:Rv84SP6.seq.:.....  
AACAGCTATGACCATGATTACGCCAAGCTATTAGGTGACACTATANAATACTCAAGCTTGCGGGTNATNGCCTTGGT  
CAACGCGACCGTGATCGGATCNGGGTTACCGCACACATNGACTGGAGCTTCCGGCAANTCATGCGCTATGCTCGCG  
GGGGGTGACGCTGACGCCNCGGTGANTTTCNGCTCNGGCACGGTGCACCGCTCNTCNAACACCTCANGCC  
ACCGGAATCAITCCNCGGCTGGCTGCACGANAGCANNTTTCNCCCTCCAAGTCTAAAGGCTGGCGANANAAGCAN  
AACGTCGCGACNAACGCATCTCTTCCNTTGTCTCTTC

## .....:Rv84T7.seq.:.....

GAATTTCTGATGGTTTGGTACACGAGCGGATCAAGCCTTCGCCGAGCCAAATCCAATCAAGAGGCCCAAGCCCGT  
ACCAATCAGCGCGGCAACGAGGGATTCGCTCATATACGCCAAATAACTGCTCTCGGGTTACACCAACAGCGCAA  
TATGGCGAAAAACGCTCCCGTTGCACGACATTAATGTCAAGGATTTGATAGTAAAGATACCCACCAACAGC  
AATCAAACTGAGAGCGGTTAAATTGACCGTAAAGCGTCCGTATCTGTTGACNGTGTCCGTTGGGTATCCGACGT  
TTCCATACGACACACCGCCGCGCATCTTGTGGATGCGTNTTGCATGGCTCATCTTTGATGATCAATCGATGTN  
GCTCAGCTCTTCGGGCATATGGAACACTCTTGGGCGGTGGAATATCAGCAATGATA

## Clone Rv85

.....:Rv85SP6.seq.:.....  
CTTTCCGCCAGCGCGCGCGGATGTCCTCATCGCTTCAGAACATCATCCGAGCTTGACGCTGTGCGCGAACAGATCC  
GCGCTGCGCGCGCGCGCGCCACACCGTTGCCGCCGATCTGGCCCATTCGCGAGGTGACCGCGCAGCTGGCTGGTCAGG  
CCGTGCGAGCTTTCGGGAAGCTCGACATCGTCTCAACAGCTTGGCGGCACCATGCCCAACAGCTGTCTAAGCACCT  
GCACCAANGACCTCGCGGACGCTTCGCTTCAACGTGGGCACCGCCACGCGCTGACCGTCCGCGCGGTGCCGCTGA  
TGCTGGAACACTCCGCGCGCGCGGACGCTGATCAACTCAGCTCCACATGGCGCGGCTGGCGCGCGCGGGTTTC

## .....:Rv85T7.seq.:.....

TGTGGGCTCCGATCCGCGCGCATGGCATGACGGCGACGCCGATCGATGACGGCCAGGCTTACGAGCTTGAGGGTGT  
GAAGTTGTGGACCAACAGGTTGGTAGCGGACCTGCTAGTGGTTATGGCGCGGATCCGCGCAGTGAAGGGCNC  
AGGGGGAATCANCGCCCTTGTCTGTCGAGGCTGATTCGCCCGGGATCACCCTGGAGCGGCGCAACAGTTTATGGGACT  
GCGTGGCATCGAAACCGCGTGAACCGGCTTCNTCGCTCAGGGTGCCCAAGACAACCTTGATCGCANGGAACGACG  
GTCTGAAGATCGCGCTGACCACACTCAACGCGGACGCGCTGTCCCTACCGGCGATCAACCGGAGT

## Clone Rv86

.....:Rv86SP6.seq.:.....  
GAGCTGGCCGAGCTGGACCGGTTACCGCGGAACTACCGTTCTCGCTCGACGACTTTCAGCAGCGGGCTTGCAGCGCG  
CTGGAACAGCGCGCACGGTGTGGTAGCGGACCTGCTAGTGGTTATGGCGCGGATCCGCGCAGTGAAGGGCNC  
CTGGCGCTGGCGCGCGCGAGTAATGTTTACACCAACCGCGCTGAAAGCCCTGAGCAACCAAGGACACCGGATCTC  
ACAGCAGCTACCGCGCTGACACGATCTGGCTGCTACCGGCTGACCTGTGCTGACCGGCAACCGCGGTGGTGGTA  
TGACCACCGAATGCTGCGCACATGCTCTAC

05673476.113000

.....Rv86T7.seq:.....  
GATCTCTGGATCGCGGGGGCTCTCCGGCCGGCCTCGGCACCTCAGCGGGCCGGCCTTCCGGCCGAACCATTCCT  
AGCCATAGATGACCCGACCTCGATGCACGGTTTGGCGGCAACGCCGGAAGGCGTCNGTCGGGCCCAAGCCGCGGCAATG  
CGGGTACCCGGGAGCGCGGGTNCGTANACANCGCTGGACTGCGTCGCGCGGTCGCTCNACNTCAAAGTCCCGGGCGT  
CCCATATCGCGATGACGCGGGCGCGCCCGGCACCAAGGGTGCCGATCCGGCCGCTCGAACACCAACCGCGCCCGCAG  
CCGCGCGGGGTCGCGCAACCCGCCCGCGCGATACCCGCTGCCCGCGTGCCTGATTGACCGCCGCGCGCACGCT  
GGCCANGGATCAAAGCCCGT

## Clone Rv87

.....Rv87SP6.seq:.....  
GGACGGTAGCCCGCCAGGCGGCTCAGGGTGCCCTTCCAGTCCACGCCGCTGTGGTCGGCGAACCGCTTATCTTCAAT  
CGAGACGATGCCAGCTTCTATCGTGTGGCGATCTTGTCCGAGGGCAGCTCGAACCGCGCTGCGAGTNCAGCCCAAGC  
GATCGTGTGCCCTTCCGCTCGACCATCTCGATACCGCAGGCACTTGCCCCCTCGAGCAGCTGGCGCGAGCCGTGGC  
AAGCAGCTCAGANGCAGATTGGACATCAGCCCTAGCCCCGCTCGGAACGGGAACCTCAGCGCAGTGGCGCAGCAT  
GGCCCAACAGACAGCAACCCAGCCAGCTTCAGAACGGTGATCGCGCCGCGGAAGCGCTCGGCGATGCGTNCACAGTAGC  
GACCTCGTCTCACTCCAGTGCCTCGGTCCAATAGAATCTTCCGCGGGCGGGTGAATCTCTGCGGATCGGGGCG  
GGCGC

.....Rv87T7.seq:.....  
GCTCGTTGCCGGCGCGATCTCTCGAGCTCGTCTTCCATCGCCCGGTGAAGTCGTAGTCGACGAGCCGACCGAAAT  
GCTGCTCGAGCAGACCGGTTACCGCGAACGCCACCCATGACGGCAGCAGTGCATCGCTTCTTGTGACAGTNGCCG  
GATCTGGATGGTCTTGATGATCGACANTAGGTCGACGGGCGGCGGATGCCAGCTCTCGAGCGCTTTGACCAAG  
ACGCTCNGTGTNNCGGGCGCGGGGTGGTGGCATGCGCGTCTGGGTCAACTCGACNATGTCCAACCGTTGACCG  
GGTTCAGTGGGGCAGTCGCGCTCGGCATCTGCAGCTCGCCG

## Clone Rv88

.....Rv88SP6.seq:.....  
GCTCTTCGATGGCTGCTTCTCGCGCTGACGCTGGCGCATCTACCCCCAGCAGTTGCTACGCGGGAGCGATGT  
CGGCGCTGTGGACCCCTCCAGGCGATGGGTCCACCCCTGATCGGCTTGGCGATGGGTGACGCTGGCGGCTACAAGG  
CCTCCGACATGTGGGCGCGAAGGAGGACCGGGCTGGCAGCGCAACGACCCGCTTTGAACGTCNCGAANTGATG  
CCAAACNACCCNCGTCTGGGTGTACTCGGCAACNGCAAGCGCTCGGATCTGGGTGGCAACAACCTCGCGGCCAAGT  
TCCTCGAGGGCTCTGTCGGGACCATCAACATCAAGTTCCAAGACGCTTACAACGCCNCTGCGGCGCACAAACCGGTGT  
TCGACTTCCCGG

.....Rv88T7.seq:.....  
GCCAGGTCGAGTCCCATCGCGCTGGGCGATTGATGTCGCCAGGAGCTCAAAANATTTGGTCCGGCGTCAGCTGG  
GCGAAAAAGCTGGCGCCAGGACTTTGCCCGAGCTGCCCGGGTTCCCGTCGCGCAGCTCGCGGCGCCGGTCAAGAA  
AAATTCGCGCAGGTGCGACACTTCGCGCGCTANGCCAGCTGCTCAGGGTGTGGGATAGAGCCCGCGGCGCGAGCG  
TGCTCGCTGTGGCGCAACACCGCATGGTCGAGAAGCGTTGCCGCCCAACGGAAATCACCTGCGTCNAANGCTTCGCG  
GCCAATCCAGCACTCGGTCGAT

## Clone Rv89

.....Rv89SP6.seq:.....  
NAAACGTTCCGGCTTNGGTGCGGGCGCTTATTTGGTCTCGGATCAACNCTCAGTCGCGGGCGGCTGCCGTTGGG  
TATNANTTGCACCGGAGCCGAAATCCGCAACNANAAGTGCNAGTAGCGGCTGCGAANTGCATCTCGCGGGAANAG  
ACTACCGGTGACACNACNACGCGCGCCGGAACAACGCACTGGCCCCGAGGATNGCGCTCTATCGCGCCCGCCCTCG  
AACTNGGAACAGACNGTGGGTTCTACCGCTGATCTGGTGGGAATGCTCNACCANACCTTCCCNANNCTACGGAACNA  
CGGCGCGATATTTCNGCNCNTCCCANCTCGAGCCTGACNCTNGATATGTCGANNCTCACCATCNCGATCNGCTGTGCGG  
GTNTTGTCTCGGACTN

.....Rv89T7.seq:.....  
CGAACGACGAACNCCNCAAGCCATGGTGGTTGGCGCGCTCAAAAGGTCCGCGGTCGCCACTACTGGAAAAATCGCCTTG  
AGGCTCNCTCGACNCCGCGCTCGAGTTGGGTCTAAGCAAAATACCTGATGCCGATCANGTCNACGCTCTCCGTCGNNC  
AAGCTGCGAGCGCGGACCACTCTACNANGTCTCGGTNCCGCCNCGGCCAGNAGCAACACAGTGACNAAATCCNTCGCGC  
NTCGGCGNAGANTCCCGGTGCNACCGNGGTGGTTCGGCGATGGTNGGTGTNCTCNNTACNAGAACCCGACGCN  
ATCANCATCGGCANACTCNCGTCGATGTGCGCGCGCGCAACCATCCCCACAATGATCNGTGGCTGCTGATCAGGCN

.....Rv8T7D4.seq.....  
CGTCACCCCCGATGCGCCCGATCGGGGGCTTCGCAGATAAAGCACGAACTGGCGGGCAAAACGTCGATCTCGGAGCCGG  
AAGGGCAATCAGCCGACCGTCGACGAACGACACCGCGCGAGACCATTAGGCAGTGACGGCCT

```

:::.....Rv9S0P6.seq:::
CTTTTCNCGATGCTCTCATGATCCNANGGAGAACNNTGCNANCNCGCCGCTGACNTNGCNCACCGCTNTGGCNGGG
TGACATTGGTGGTGGTGGTGGCGGGCTGCNACCGCGCATCGANGCGCAGNCCATNTTTTGGCGCCGACGCGTNTTGTCTC
NACCACGANNCCCAATCTCNCGCCGNCNCCGGTGGANCTACNCGTNTCTTGCCTACTCTCTCGATNTGGCTCNCGNNTTC
GNCACGCTNTGGTTTGGTNACTGCTTACTGCTTGGTCT

```

[illegible]

CTGTGTGGCGGNCGGCGGATCTCGGCTTTTACTAACCGAACCCGATGTGGGCTCCGATCGCGCGCGCATGGCATCT  
ACNCGGACGCCCGATCGATGACGCCGACCGCTACGAGCTTGRAGGCTGTGAANTTGTGGACCNACACGGTGTGTAGCGG  
GACCTCGTANTGTTATCGCGCGGCTACCGCGCATGAANGGACCGCGGGGGAATCANCCTGCTTGTCTGATCGT  
GATTCTCGCGGGATCACACNTGGAGCGCCNCINANTTATGGGACCTGCTGGCATCGCAANA CGCGCTGACCGGCTTCA  
TCNCTNCGGTTGCCAAAGCAACTTGTATCNCNGGAAGCGAGCTCTGAANATCGCGCTGATCNCNACTCACACGCGG  
ACCGTCTCTACGGGCGATCGCACCGGANTTGCCAANC CGCGCTNANNATNCGCGNGAATGNCCTGCCACNANTGCAT  
GG.

.....Rv91T7.seq:.....  
TGGGGTGC CGGGCGCGCGAGTTCGCTCGCTGGGATCACGCAGAGTCGCCGCGGGCTGCCGTTGGGCTATGAATTGCACC  
GAGGCGGAAATCCGCANCAAATCGCATAGCTAGCGGCTGCAGAAATGCANCTTCGGCGAAACCGAGTACGGTGGACA  
ACGAAAAGCGCGCGCAACNACGCACTGGCCGAGGGATTGGCGTCAATCGGCCCGGCCCTGCAACTTGAAGANAC  
ATTGCGGTTCTACCGTGATCTGGTGGGAATGCTCCAAACNNACCTTCNCGAAAGCTACGGAAGACNACCGCGCGCATNTT  
CGCGCTTCCCAGCTCGAAGCTGACGCTGAAATCG

[illegible]

```

.....:Rv92T seq:.....
GGACACTGTTTCGCGTCCCTCGTCAAAGCCGGATGGTCTGCTGCGCGGACCCGACCCGACCTTCAGCGGGGGTT
CAGACGTCGCGGGTGGCTACTTCCGATCGCGCAGTGTGGCGTGCCTGTGGTGATGCTGAACCTCACCGCGTT
GACTTGGATCGGTTTCGGGATCTGGCTGTGGCGGACCCGCGATTATGTGCTGCTGACGGCGCGGCATCGCGGCA
TGGCCTTTCGGGACGNCNANANACGCGACCCGGAGTGTGAACTAGCTGTCGCGCGGTATTTACAAATTCGNTTATA
TGCTACACATAAGACGCAAACTCTGTTATGTCAANTCGCTGAGTGTGGCNCAAGAATGTGTTGG

```

05673475 113000

TCTCTTCGCGTATCGGTTGGGCTGTACCAACAGTTGGTAGTTCCTTCAAGTNCCTGTTGTTCAAGCGGTACAGCGGTGCG  
 CGCGCTGTCNANGTCCNCCGGACGGCGTATCCC GCCAGGCGCGGTACAGGTCGCCCTTCCANTCCACGCCGCTGTGGTGGGGC  
 AACTCGTNATCTTCATTCAGCATCATCGGACGCTTCATCCTGTTGGGAGATCTTGTTCNACGGGCACTTCNAAACCGGGCTG  
 NCTAGTACNCCACNCGATCATTCTTNCCTTCNCTGNCACATCTCGATNCNCTCAGCTTCCTCCCTCGANCTCGTGGGC  
 CGAGCGCTTGGCANTACCTCNGAGCCCCATTGGACATCANCCANCCCGCCTCGCGAACGGGAACGTCAAGCNCTCGG  
 CGCAACCTGGCCCAACN

:::::::::::Rv947T::seq::::::::::::  
 CACNCCGTCATCGNAGCCCCNCTGAAGATNGTTAGGACGCTGGTGGCGGCGCTCGTTGCCGCGGTTNATCTCTGTCGA  
 GCTCINTCTTCATCTGCGCGCGGTGAAGTGTCTCGACNAGCCGACNAAATGCTGCTCNAGGACGCCGTTACCNKNA  
 ACNCCNCTCNTGACNCGACCACTGCNCTGCCCTTCTTGTCACGTACCCGCNATCTGGATGCTCTGATGATCNAC  
 TANTTGTGTCACGCGCGCGCGATGCCCATCTCTCNAGGACCTTTGACGACGCAGCNCTCGTGTATCGGGCGCGCGGG  
 TTNTNGTCGATGCGCGCTCTGGGGTCACTCNACNATTTCAACCCTGTACCCGCGGCTTCA

```

:.....:Rv95SP6.seq.....:
TGGCCCTTTTGCNATGGCCNCAATNNCGCTATNGCGAGCGTGAACCATCATCNTCCNGGCGACTGTGGCCGTGANC
CGCAAGGGTNGCCTNAGTCNTCCTCTGNGGCATGGTTNCCACACGGAATGNCGGTAAGTCTGGTGGCGAACCTGGCC
CGCTCGGGGTGGGTTCGGATTGCTCGGTCATNAAAGGTGCTGCCCTTGGCTGACNACNATCNCNATNATACNTTNC
GGGATGNGCTCCCGCATCTNCGCTCGCGGNGCGGATCNCCTTGCNACGACGCCACCGGAATCNCAGNTGGC
TCATCGGGCTTACCGGCCATCTTCCCCGGATTCTTCGCGGCNNGTNCNGGGGACCCCGGACTGTGACNGGCCAA
CGGGCTCATCATCG

```

```

:::Rv95T7.seq:::
CCGGAATCCGGGTGTCTGAATCTTCCGCTGCTTCCCTTCANCGCATTGAGCTTCAGCCCGACCGGCAGGTNNNGAGTCGGC
ATAGCGTCTCTTCCGCCGCCACCGCTGGCTAATATNCACACCCCGAGCGGGTCAGGGTCTTTGCACCGGGACGACGC
ATACCGGCAGCGCAACATCNCGGCGGGTGCAGCNTGAACGTCCAATACCANTCNAACAGTGTCCGCGCGTNAAAAC
CCGANCCGGCGGTGCTCTNCGTATCAACGGCTCTTGCGCAACAGCTGCAAGTGTGCGGGTGCCACCGCGCTTGACGA
TCTTTGATCTTCGGANCTCGGCGACAGCTCGACCGCCGGGCA

```

```

:::.....:Rv96SP.seq:::.....:
CTCCCGCAGCACATACAGCGAAGTAATGGCAATTCACGCGAGCATTACTCTACGCGCGCAATTACGAATTCACACA
CTCGGGGCAGCTGGTGTTCGATAACGAAGTATCTTCAACCGGGTTGAGTATTGAGCGTATGTTTGGAAATAACAGCGCGAC
GCTTCATTAATTAATCTCCACCGCTGGTTTATGATGACATCGTCAAAATTTTCATTGACAGCGATTCCCAATTAAGAAG
AGCAATTTCCGAGGACAGATTTGAAGAGCTTGATCAATGGCTGTGTCAAAACAGATTCCTACCGGTCTGACCTTT
ACCAACTCATCTCGGTTTACCTACACAACTTTTGAAGACCATGCTCCCGAGGCATCCGAATTTGCTGCTCATCA
CGGGGACTGAGAGCGTTTACTACTTGTGCTAATTTGGTGAAGCAAAATACGT

```

```

:::.....:Rv9S9P::seq:::.....:
CTTCACNTCCGTACCGCTCGGGTACGCTTCGGTNCATTTGTGCGAGTGTAGATGACGACCGGAGCTCGTGGCGATC
TTCATAGACGCCGCCGACACCTTCAGTTGCTACACGGAAATCCAAACCGGTANAAGGTGGCGGANGCGTCNGCATTGTCAT
CGGGATATGGCGCTCGGGAGCGCTCAGAGCCCTCGGGCGTCCGCGACGACATCCGACAGCTCGTGGGGTGGTCCGACGG
CGCATGGSCGACCATCGCATTCACCAAGCTTCGGGCAATTCACGACAGCTANAGCATGGTTCCTTCTTAAGAACACCGA
ANTTTCAGGACCCGAATGCTCCGGGAAACATGTCACGGTAGTTCGGTATTCGGGCTACCGGCTGANCATTAGGACCGG
CGGCGACACCGCAGTCACTACAGGACATCAGCCGCCCGCCGACACGACCGGCG

```

:::::::::::Rv9T7.seq::::::::::::  
 CAGGATCGCAAGCTTGTATGCCGCCGAAACCGAGCGTGAGCAGCCGCGACGCCACACGCGCGCTCGGGCGCGGGCC  
 CGGCGCGCCAGGCTGCTCGCTCGGTTGATGCACGCCACCGCGACACACCGCGCTCGGCTACGTGAGGCATACCGG  
 GCGGAGCTACATCGGCTCGGCCGCCAGTGTTGCGGCCCTCTTTCGAGGTCGAGGTCGATACCGATTTCGCATCCGC  
 AGCCGACCCCTGGACGACAGAACCTGCGCCATCAAGATTGCTTTGCGGGCGGGGCGAAAGAACCACTTGCATCTCGGC  
 GCAATTGGCGCGCGCTGCTGCTCCGAAGAGGACCGCTCTCGGTGCTGAT

21.06.00 ART 34 AMDT

123

**Table 4 :** End-sequences of the polynucleotide inserts cloned in the named recombinant BAC vectors contained in the I-2049 *M. bovis* strain Pasteur genomic DNA library.

RvXXXSP6 corresponds to the SP6 end-sequence of the clone RvXXX.

RvXXXT7 corresponds to the T7 end-sequence of the clone RvXXX.

RvXXXIS 1081 corresponds to a region located close to a copy of the IS1081 repetitive sequence (Insertion element).

The character « - » denotes an uncertain base residue.

#### Clone X0001

.....X0001SP6.seq:.....

AAG-

TCCGGTTTCCACACGCGCGGTTGACCTAGTCATATGTAATCATGTGTACCATGTGCGGGCGCTTTTCGACGGCCG  
CGAACCAACCGGA-ATTTCCTGTGATTTCACTGCATGCGTACCATCTGGCACAATTGAGCA-TTGTCT-  
TCCGGTGTGTCGG-CGGGTTGCGTGC CGCCTGCTGCGA-ATGCAACA-  
TAAGCCCGAACCCACCGGCTTGGTGACCAACCGCAGCTGCGTGTGGGGGTTAACCACTCCGCGACCCCAAGGATGGT  
CATTTCCAATGAACCGGCTGGACTTCGTCCA-A

.....X0001T7.seq:.....

GTCCGGTTTCGATCGACCGGATCTTCACCTCGTAACCTCGATGCTTAGCAGGATCCAGCTTGACCGGTTTGGCTCT  
ACCCACTCTTTGAGTGGCGCGCTCGCTGTGCCCCATCGGTGTTTCATGACGAACGCTTCGAAAGACTTCCTTTGTG  
AGCCGGAATGTCTGCGTAAGAAGTTCATGTCCGGGAAGTAGACCCGCTCGCCCTCCAGCTGTAATCCTTCGAGG  
TCCGCTTCTCGCCGGATCCGATAAACACCGGCCCCAGGCACCGCAGCGTGAGTTTGAACGGCTTCAGGTAGGTGTT  
ATGCGCGGACTCCGGGAGTGCAGAAATAGCGGTGCGCGTAGCTGTAGACCGGATGTTTTCGCCCGAGGCTGACG  
TCGAAGATGCTCCTTGGAAAGGGCGCGA

#### Clone X0002

.....X0002SP6.seq:.....

AACCTCAAGTTTTTACGGTGATCGCGCATCACTTGTTTCATGAACCTGGAAGCAGCGCAGCGCTTCTTTTCGCCCGCA  
ACATGAGCCAGCCTCTCGTCGGCGGTGCGGGTGCAGGTGCTCGGGCAGCTCGGCGCGACAGCCGCTTGACCTGAAA  
CCAGCTTCCATATCCCGCGAC-  
AACGACGCCAGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCGTTCTCCACGACCGGGCCCGG  
TGT

.....X0002T7.seq:.....

GTCCAGGTTTCGACAAATGTGGTGCCGGTTTCGGCGGCTACGTGCCATCGAGACACTGGCGCA-GCTATCGACCCGTT  
ATCGGCTGCGAGCAATCGCGTATGCGTCTTGTGACATGAGTCGCGCAGCGCTCGTCATGGTCGACACCCACGACGG  
AAAGACGCAGATCGCCGTCAGCGTGTGCCCGGATTATCAGGACTGACCTCTGGCTGACCGGCATGTTTGGTC  
GCGATGCTTGGCGCCCGCGCGGTGGTCGTGGTCCGCTCGGATAGCGAGTCAAGCAATCTCTGTGCACTCGAA  
AGGGTCTCGCGGTGCCGTT

#### Clone X0003

.....X0003SP6.seq:.....

TTCGAGTCATGCGCCGCGCTCGACCAAGAA-ATGCAGTCG-  
GGTTCGATCGACCCGATCTTCACCTCGTAACCTCGATGCTTAGCAGGATCCAGCTTGACCGGTTTGGCTCTACCCA  
CTCTTTGAGTGGCGCGCTCGCTGTGCCCATCGGTGTTTCATGACGAACGCTTCGAAAGACTTCCTTTGTGAGCGG  
GAATGTCTGCGTAAAGAGTTCCATGTCCGGGAAGTAGACCGGTGCGCCCTCCACGTGGTACTCCTTCGAGGTCCG  
TTCTC

::::::::::X0003T7.seq::::::::::  
GTCATGTGTACCAATTTGCGGGCGCTTTTCGACGGCCGCGAAACACCGGAGATTTCTGTGATTTCAGTGCATGCGTA  
CCGTCTGGCACAAATAGACAGTTGTCTGTCCGGTGGTCGGCCGGGTTGCGTGCCCGCTGCTGCGAGATGCACCAAT  
AAGCCGAACCCACCGGCTTGGTGACCAACCGCACGCTGCGTGTGGGGGTAACACGCGCCGACCCCAAGGATGCTC  
ATTTCCAATGAACCGGCTGGACTTC-TCAACAA

## Clone X0004

::::::::::X0004T7.seq::::::::::  
AACAGCGCGGTTGAACATGATAGTGCAGCGGCTCGAGCAGGCGGGCCATTGTTCGATGCGGTTACCGAAAGAT  
CTCTTCGGTGACCTGCCCGCCGCCAGCTCGGCCAGTGCCCGGCTTGCCCGCCGGCGGACGATCTTGCGCT  
CCACGGTGGTCGGG

## Clone X0006

::::::::::X0006T7.seq::::::::::  
GCATCTGGGCTGGCGGTGGTTCGCCGCTCCGAAGCCGTGGAACACCATCGCCAGCGCGGCTTCCACATCAACGACCA  
TTTCGGCCAGCTTGCAGCGCATCAGCGGCTTGTGATGAGCGCCCAACCAATGCCCGCGCTGCCCGGCGTA-  
CACACGATTCGACCAAGCGCGCGCGGCTTGCCGAGGGCGAAGCAGCGGTGCCAACCGCAATCTGTTGGTCAG  
CTCCATCATCGGSGTGAGTCCTTGCCG

## Clone X0007

::::::::::X0007SP6.seq::::::::::  
ATCGGTTTCCAGCAACAGCCGATCGACGGCTTCGCCCA-  
GGCCGCTCCCGGGCGACCCGACCATTTGCTGTCCGCGGTAACGCCATCAGCGGATGACGCGAGTTCGTGCTGTCTA  
GCTCCACCATCGGCTGCACACCGCGGCCAG-ACCCATTGGCGGTGCGACTCGTA-  
AGCAGGTAATCCTCGTGACAGGACTCGGTAAACACCGCGCGGAGCTCCGTGCCAGTTCGCGGGGTTGACACCGGC  
GGGCTCGGGATGGACGACGACGCGGTGCTGACGCGCCTGTG

## ::::::::::X0007T7.seq::::::::::

AGCGGTTTCCCA-  
GCGGGATGTGCTGTAGAGCGCGCACACACGCGCCGACCTAAGGATGGAACGCGCGCATCTTCTGACGCGTAACC  
GCGTTGTGATCGCGAGCTGAGGAGACGGTATGGGGGAGGGTTCTCGGAGGCCATCTGGGATGTTGATGTCTGCGAT  
CTTGAGCGGTTGCAACTCGTCGCGCGGACGGTACGCGGACGCGCGAACCGCGTACCACCGTGACCTTCTGAGGA  
AACGCTGCGTGTGGCTACAGAGATGATGTTGGTCACCCGCGAGCTGGATACCGAATTGTCATCTGCACG

## Clone X0008

::::::::::X0008SP6.seq::::::::::  
CRAAGCTTCCACAGGTAGGGATCGAGGAACAGCGGTTGAATGATAGGTGCGGCCGGCTCGAGCAGGCGGGCATT  
TGTTGATGCGGTTACCGAAATCTCTTCGGTGACCTGCCCGCGCGGCGAGCTCGGCCAGTGCCCGGCGTTGGC  
CGCCGCGGCAACGATTTGGCGTCCACGGTGGTCGGGGTCATGCCCGGAGCAGGATCGGCGAGCGGCGGTCAGCC  
GGTGAACTTCGTGCAAGCTTGACCTGCCGTGCGGGAGGCGAACACCGGTGCGTGCGTANCTCCACCAAGCCCGG  
GCAACTCGGGGGTGGCGCC

## ::::::::::X0008T7.seq::::::::::

TGGACCTCATGACAACGCGGGCGGATACCCCGCTACGCCAGCAGCATGACGGCGGTAGCGAACCACCGCGGAT  
CGAGCGCAGGTGCGTGCATGTGCTCAGCGAATCGCCCGCGCACCGGATCTCGAGGATCACCAGTGCCACCCCTGC  
AGCGCGACACGACGATTCCTGATCCACCGCCACGCGCATGCGGCTATATGCGGCGGATGGTG  
ACGATGGCCAGCGCCACATACATTGTGGCGGCCAGAACACCGGCTTGGGGCGCGGTCGATGAACACTAGGCGAGC  
CAGATCGCCCGGGTCAACAGGTTGACCATCAGAAAGCTTCGCA

## Clone X0009

::::::::::X0009SP6.seq::::::::::  
TTTGGTGGGCGCGCAATCAACTTC-GTCT-  
CAGCGGTTTCCAGGCGGGATGTGCTGTGAGCGCCGACCCAGCGCGGACGCTAAGGATGGAACGCGACGGATCT  
TCTGACCGGTAACCGGTTTGGTATCCGAGCTGAGGAGACGGTATGGGGGAGGGTTCTCGGAGGCCATCTGGGATCT  
TGATGCTGTGTCATCTTGAGCGGTCGCACTCGTCGGCCGCGACGGTACGCGCAGCGGCGAACCGCGTACACCGGT  
GACCTTCTCAGGAAACGCTGCGTTGGCTCTACGATATGATGGTGGTCACCG

.....X0009T7.seq.....  
CGCCAGGGCCGCTCCGGGGGACCCGACCATTTGCTGTGCGCCGCTAACGCCATCACGGATGACGCGCAGTTTCGTCTG  
CTGTCTAGCTCCACCATCGCTGCACACCGCGGCCAGGACCCATTGGCCGTGCGACTCTAGAGCAGGTAATCCTC  
GTCGACCGATCTGGTTAACCACTCCGCCCACTCCGCTGCCAGGTCGGCGGGGTTGACACCGCGGGCATCGGGATGG  
ACGACGACCGCGGTGCTGACGGCGCTGTGCGCAGCTGAGCTCGGACACAGCTAGTAATGTAGCTTAACCTACTTA  
ATGGGTGCGACGCCCGGGGCTGTCGCATGTCACACGTTGCTCGACTGGAAGAAATGCTCGTCGGGGAGCAATG  
GCACC

## Clone X0010

.....X0010SP6.seq.....  
AATACTCATCTTGATCGGTTCCAGCAACAGCCGATCGACGGCTTCGCCAGGGCCGCTCCCGGGGACCGCGACCA  
TTGCTGTGCGCCGCTAACGCCATCAGGATGACGCGCAGTTTCGTGCTGTCTAGCTCCACCATCGCTGCACACCGG  
CGGCGAGGACCCATTGGCCGTCGACTCTAGAGCAGGTAATCCTCGTCGACGGAATCGGTAACCAACCGCCGACG  
TCCGCTGCGAGCTCGCGGGGTTGACACCGCGGGCATCGGATGGACGACGACGCGGTGCTGACGGCGCTGTCGC  
GACTCTGAGCTCGG

.....X0010T7.seq.....

GGATGTGCTGTGAGCGCGCGACCAACAGCGCCGACGCTAAGGATGGAACGACGCGCATCTTCTGACGCGTAACCGG  
TTGTGATCGCAGCTGAGGAGACGGTATGGGGAGGGTTCCTGGAGGCCATCTGGGATGTTGATGTCTGTCGATCTT  
GAGCCGGTGCAACTCGTCGCCCGGACGGTACGCCGACGGCGCAACGCCGCTAACCCGTGACCTTCTGAGGAAC  
GCTGCGTTGGCTCTACGAGATGATGGTGTGTCACCCGCGAGCTGGATACCGAATTCGTCAATCTGACGCGCCAGGGG  
AAGCTGGCGTTGTACACGCCCTGTGCGGGGAGGAACCGCGCAGGTGGGTGCGGGCGGCTTGCTACGCAAAACCGA  
CTGTTGTGTC

## Clone X0012

.....X0012SP6.seq.....  
ATCAGCAACAGCGACGCTGTGTCGGATCAGCGCCCGCTGCGGGGCAATGTTGAGCGCTTCTGCTCTGGTT  
GAGGCCGCTGGGAC-  
CCGAGTGGCTCGTCGGCCATGGGCGACACACACCGTGGTGATGCATCTAGACGTGCAGGACCGTCCCGCTGGC  
CTGCA

.....X0012T7.seq.....

CGCGTACGTGCCATCGAGACACTGGCGAGGCTATCGACCCGTTATCGGCTGCGAGCAAAATCGCGGTATCGGTTT  
TTGAGCATGAGTCGGCGACCGTCTGTCATGGTCGACACCCACGACGGAAGACGAGATCGCGCTCAAGCATGTGTGC  
CGCGGATTATCAGGACTGACCTCTGGCTGACCGGATGTTTGTGCGCATGCCTG:

## Clone X00013

.....X0013T7.seq.....  
TACAAGCGGCACCTCGCCGGTGAACCTGACCGTTTCGACGCTGCGCACCGCCCGCGGGCGGCTGCTCGGCGCGCCGGC  
GGCCCCGAGGCTGAGAGGGGAACCAACATGCAAGTGAAATGACGGTAAACGGCGAGCCCGTCAACCGCGAGGT  
CGAACCCCGGATGCTGCTGGTCCATTTCTCCGTGATCAGCTGCGGCTCACCGGAATCTACTGGGGCTGTGATACCA  
GCAACTGCGGGACATGCTGGTGGAGGTGCGACGGCTGCGGTTGAATCTGCACGATGCTCGCGTGTGCTGCTCC  
GGG

## Clone X0014

.....X0014T7.seq.....  
AGCGGCTGGTTACGACTCCCTGTTTGTGATGACCACCTTACCAACTGCCCATGTTGGGACGCCCCG-CC-  
TCGGATGCTGGAAGCTACACTGCCCTTGGTGCGTGCC-C-GCAGCGAGCGGCTGCAACTGGGCGC-  
TTGGTGACC-GCATACCTACCGACCCC-ACCCTGCTGG-CAAA-  
ATCATCACACGCTCGACTTGGTTAGCGCGGTCGA-CGATCTCGGCATTGGAACCGGTTGGTTT-

## Clone X0015

.....X0015SP6.seq.....  
ACGCGCGCCGATCATATCTGCTATGGATGTACAATTGAGCTCTTGTGCTTATACCACTGATGTTGGGACGCCCCG-CC-  
CTATGCTGAGCTGTGATGCGGGAATCGGCCCTGGCTCGACTCGCGCGGGCTCTGGCTGATCCGACGCGGTGCGCG  
ATTCTGGTGGCGTTGCTGGATGGGCTTTGCTATCCGGGCGAGTACCTGCGCACTCGGGTTGACCCGATCGAATGT  
GTCCAACCATCTGCTGTTTGGCGGGGCTGCGGGCTGGTA-TCCCAACCTATGAGGGCGGGCAGGTTGCGTAT

::::::::::X001077.seq:::::::::::::  
 CGAACCT-AATTGTCTGTATGCCAGCTCACCAA-  
 GCATGCGCTGGTGGCGGGCGGTGAAGCCGGCGTCTGGCGACCCTCCAATC-ATGTGGAT-  
 GCCGGAATGGGGATGTCCGG-ACGGCGAATCCGTA-  
 TTCCGTTTCTCCGTCGAGGCCAGGTGGATGGGGGGAAGGATC-TGGTGTCCGGGATGAT-  
 ATAGGGGGCATGCGCGCGGTTGAAGTCACTGATCGGAATTCGGGAATCGTGAT-CCGACGTTCAAGGCGAAC



## Clone X0019

.....X0019SP6.seq.:  
CTAACGGAATGAAAGCCCTGGTGGCCGT-  
TCGGCGGTGGCCGTCTGCGCACTGCTCGGTGTATCTTCCGCCCAAGCTGATCCCGAGGCGGATCCCGGCGCAGGTGA  
GGCCAACTATGTTGGCCCCCAAGTTCCCACTGCTTGTGATCACACCGAATGGCGCA-  
TGGGGAATTTCTGCCAGCCTCCGGGTCTACCCGTCCCAAGTTGGGCGTACA-  
CCTCCCGCGCTCGGGATGGCCGCTGCCGACCCGGCTGGGCC-  
AGGTTCTCGCGCTGTACCGGAAGCCGACACTGCCGGC

.....X0019T7.seq.:  
CCGCGGGACAC-CCCTC-

ATGCTGCGCCATGGACGGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGCTTCGCGCGCGG  
CGTGACCCGATCCCGTTGACCGGGCGGATCGCGGTGATCGTATGACGGCATCGCCACCGGAGCGACGGCCAAGG  
GGCGTGGCAGTCCCGGGCGCACGGTGGGACAAGTGGTGTGCTGGCGGTCCCGATCGGCCA-  
ACGACATCGTGGCGAAGATTCCCGGGTACGCCGATGATGTGGTGTGTTTGGCGACCGCGCGTGT

## Clone X0020

.....X0020T7.seq.:  
CTCTGGGACCGGCCACGGTGCC-

CCGGCGTTCCCGGACGTGCTGCGCCAGGTGCCGGCGCGCGTGCATGTTGTTCCCGGATCGGCGCGTGCCAGAG  
CCCACCGGTGAATCTGGCGCTGGCCGACACCGTGCCTGAGGCTTGCATCGTGCAGCGCTGGCGTGGCCAGGA  
CGAGATCCCGACGGATTGGGCGAGATGCGTGCTACCATCGGGATATTGACGGCGTGACCCGGGCGACGCCGAAC  
TGATCGCGCACCGGTCAAAGCGCGC

## Clone X0021

.....X0021SP6.seq.:  
AATACTCAAGCTTTCGTCACTTTCGCGCCAGCAGACCAACAA-AGCATCGGGACATACGGA-

TCACTACCCGGCCAAAGGTGATTTCTTGGCCGCCGTGACGGCGGCAACGACGCCAGCGACCCAC-  
TTCAAGCAATGGCCA-CGCGTGGCGGGCCAGAGGTGGTGTGCTCGCGGCTACTCCAGGGTGGCGCGTGATC-  
ACATC-TCAACGCCGACCACTGCCCGGCCCTCGGGTTACGCGAGCCGTTGCCCGCCGAGCGGAC-  
ATCATATCGCGCGATCGCCCTGTTCGGGAATCCCTC-GGCCGCGCTGGCGGGCTGATTAA

.....X0021T7.seq.:  
TGGCGCGGATTTGGCTGGCTGCCCAATATTCAGAATCGGGCTTTCTTTTTCGCGGACAATAAGGTACAGTAAAC

CTCGTTTTGTGAGATGCGGGCGGGGCCGGCGAA-  
TCGACCTCGAGTGAATGGATCTCGAGTGAATGGACAGGCGATCGCTACGAGTGCATCCCCATCAACAGACCGGT  
GCTCTTGATCGGACCTGAAGGTCCCGCACGAGGGTGTGGTTGCCGGCGGGGTACCGGTGCGGTAGCGACGTA  
GTGTTTGAACGAATTTCTTGATGCTCAACCTGTTTGGTGTTCATCAAGTTCT

## Clone X0175

.....X0175SP6.....

AA-CTTGCGCGCTCGGCCGGGTC-AGCATCCAGCTGCTCGGCAAGGAGCCAGCTAC-C-  
TCGCTGCGTATGCCAGCGGTGAGATCCGCCGGGTC-  
ACGTCGCTGCCGCGACCGTCCGCGAAGTGGCAATGCCGAGCAGGCAACATCAACTGGGGCAAGGCCGGTCCG  
ATGCGGTGGAAGGGCAAGCCCGCTCGGTCCGGGCGTGGTGAT-AAACCGCTC-  
ACCACCGCACGCGGCTGGTGGGGTAAACCTCCGGCGGCGCTACCCGGTTAGCCCGTGGGGCAA

.....X0175T7.....

A-TGGAAGTGACACTCTACCTTGAAGTGCATACCGCCGACCTATGCTCGGATAGCTCGGCGGAAAGAAACG  
CTTGCACTGCGCCGAATAGCGGCTACGTCGTGAGCGCCATCACTCTCGCGCGAGTGATCGCCAGCTGGGCG  
GCGCGCAGCTGACCGTGGGATTCCGGTGCGCCCGCGGCAACGCGCCGATCGTGACCCGCAAGCAATCGG  
GCGATGTTCTGAACGCTGCATAGGCACTCCCGCGCGCTGGCAGGCCAGTGCGAACCGCGCGGTGCTCCG

## References :

- Altschul, S. F., W. Gish, W. Miller, E. W. Myers, and D. J. Lipman. 1990. Basic local alignment search tool. *J. Mol. Biol.* **215**:403-10.
- Balasubramanian, V., M. S. Pavelka, Jr., S. S. Bardarov, J. Martin, T. R. Weisbrod, R. A. McAdam, B. R. Bloom, and W. R. Jacobs, Jr. 1996. Allelic exchange in *Mycobacterium tuberculosis* with long linear recombination substrates. *J. Bacteriol.* **178**:273-279.
- Barany F., 1991, *Proc. Natl. Acad. Sci. USA*, **88**:189-193.
- Bensimon, A., A. Simon, A. Chiffaudel, V. Croquette, F. Heslot, and D. Bensimon. 1994. Alignment and sensitive detection of DNA by a moving interface. *Science* **265**:2096-2098.
- Bergh, S., and S. T. Cole. 1994. MycDB: an integrated mycobacterial database. *Mol. Microbiol.* **12**:517-534.
- Birnboim, H. C. and J. Doly. 1979. A rapid alkaline extraction procedure for screening recombinant plasmid DNA. *Nucleic Acids Res.* **7**:1513-1523.
- Burg J.L. et al., 1996, *Mol. and Cell. Probes*, **10**:257-271.
- Cai, L., J. F. Taylor, R. A. Wing, D. S. Gallagher, S. S. Woo, and S. K. Davis. 1995. Construction and characterization of a bovine bacterial artificial chromosome library. *Genomics*. **29**:413-425.
- Canard, B., and S. T. Cole. 1989. Genome organization of the anaerobic pathogen *Clostridium perfringens*. *Proc. Natl. Acad. Sci. USA* **86**:6676-6680.
- Chu B.C.F. et al., 1986, *Nucleic Acids Res.*, **14**:5591-5603.
- Chuang S. et al., 1993. Global regulation of gene expression in *Escherichia coli*. *J. Bact.*, **175**(7) : 2026-2036.
- Chuang, S., D. L. Daniels, and F. R. Blattner. 1993. Global regulation of gene expression in *Escherichia coli*. *J. Bacteriol.* **175**:2026-2036.
- Cole, S.T., R. Brosch, K. Eiglmeier, T. Garnier, S. V. Gordon, C. Churcher, D. Harris, K. Badcock, D. Basham, D. Brown, T. Chillingworth, R. Connor, R. Davies, K. Devlin, T. Feltwell, S. Holroyd, S. Gentles, K. Jagels, J. McLean, S. Moule, L. Murphy, K. Oliver, J. Osborne, J. Parkhill, M. Quail, M-A. Rajandream, J. Rogers, S. Rutter, K. Seeger, J. Skelton, R. Squares, S. Squares, J. Sulston, K. Taylor, S. Whitehead and B.

- G. Barrell. 1997. Genome Sequence of *Mycobacterium tuberculosis* H37Rv. *Microbial Comparative Genomics*, 2:174.
- Collins, D. M., and D. M. Stephens. 1991. Identification of an insertion sequence, IS1081, in *Mycobacterium bovis*. *FEMS Microbiol. Lett.* **67**:11-15.
- 5 Cousins D. et al., 1998, **36(1)** : 168-170.
- De Wit D. et al., 1990, *J. Clin. Microbiol.*, **28** : 2437-2441.
- Dear, S., and R. A. Staden. 1991. Sequence assembly and editing program for the efficient management of large projects. *Nucleic Acids Res.* **19**:3907-3911.
- Duck P. et al., 1990, *Biotechniques*, **9**:142-147.
- 10 Guatelli J.C. et al., 1990, *Proc. Natl. Acad. Sci. USA*, **87**:1874-1878.
- Kievitis T. et al., 1991, *J. Virol. Methods*, **35**:273-286.
- Kim, U. J., B. W. Birren, T. Slepak, V. Mancino, C. Boysen, H. L. Kang, M. I. Simon, and H. Shizuya. 1996. Construction and characterization of a human bacterial artificial chromosome library. *Genomics*. **34**:213-218.
- 15 Kwoh D.Y. et al., 1989, *Proc. Natl. Acad. Sci. USA*, **86**:1173-1177.
- Landegren U. et al., 1988, *Science*, **241**:1077-1080.
- Liu, Y. G., and R. F. Whittier. 1995. Thermal asymmetric interlaced PCR: automatable amplification and sequencing of insert end fragments from P1 and YAC clones for chromosome walking. *Genomics*. **25**:674-681.
- 20 Lizardi P.M. et al., 1988, *Bio/technology*, **6**:1197-1202.
- Matthews J.A. et al., 1988, *Anal. Biochem.*, **169**:1-25.
- Michalet, X., R. Ekong, F. Fougerousse, S. Rousseaux, C. Schurra, N. Hornigold, M. Vanslegtenhorst, J. Wolfe, S. Povey, J. S. Beckmann, and A. Bensimon. 1997. Dynamic molecular combing - stretching the whole human genome for high-resolution studies. *Science*. **277**:1518-1523.
- 25 Misumi, D. J., D. L. Nagle, S. H. McGrail, B. J. Dussault, Jr., J. S. Smutko, H. Chen, O. Charlat, G. M. Duyk, C. Ebeling, L. Baldini, G. A. Carlson, and K. J. Moore. 1997. The physical and genetic map surrounding the *Lyst* gene on mouse chromosome. *Genomics*. **40**:147-150.

- Pavelka, M. S., Jr., and W. R. Jacobs, Jr. 1996. Biosynthesis of diaminopimelate, the precursor of lysine and a component of peptidoglycan, is an essential function of *Mycobacterium smegmatis*. *J. Bacteriol.* **178**:6496-6507.
- Philipp, W. J., S. Nair, G. Guglielmi, M. Lagranderie, B. Gicquel, and S. T. Cole. 1996a.
- 5 Physical mapping of *Mycobacterium bovis* BCG pasteur reveals differences from the genome map of *Mycobacterium tuberculosis* H37Rv and from *M. bovis*. *Microbiology.* **142**:3135-3145.
- Philipp, W. J., S. Poulet, K. Eigmeier, L. Pascopella, V. Balasubramanian, B. Heym, S. Bergh, B. R. Bloom, W. R. Jacobs, Jr., and S. T. Cole. 1996b. An integrated map of the
- 10 genome of the tubercle bacillus, *Mycobacterium tuberculosis* H37Rv, and comparison with *Mycobacterium leprae*. *Proc. Natl. Acad. Sci. USA.* **93**:3132-3137.
- Poulet S. et al., 1995, *Arch. Microbiol.*, **163** : 87-95.
- Ross BC, 1992, *J. Clin. Microbiol.*, **30** : 942-946.
- Sambrook, J., E. F. Fritsch, and T. Maniatis. 1989. Molecular cloning: a laboratory
- 15 manual, 2nd ed. Cold Spring Harbor Laboratory, NY: Cold Spring Harbor. N. Y.
- Sanchez-Pescador R., 1988, *J. Clin. Microbiol.*, **26**(10):1934-1938.
- Segev D., 1992, in « Non-radioactive Labeling and Detection of Biomolecules ». Kessler C. Springer Verlag, Berlin, New-York, 197-205.
- Sheng, Y., V. Mancino, and B. Birren. 1995. Transformation of *Escherichia coli* with
- 20 large DNA molecules by electroporation. *Nucleic Acids Res.* **23**:1990-1996.
- Shinnick T.M. et al., 1987, *J. Bact.*, **169**(3) : 108-1088.
- Shizuya, H., B. Birren, U. J. Kim, V. Mancino, T. Slepak, Y. Tachiiri, and M. Simon. 1992. Cloning and stable maintenance of 300-kilobase-pair fragments of human DNA in *Escherichia coli* using an F-factor-based vector. *Proc. Natl. Acad. Sci. USA.* **89**:8794-
- 25 8797.
- Spargo C.A. et al., 1996, *Mol. and Cell. Probes*, **10**:247-256.
- Stone B.B. et al., 1996, *Mol. and Cell. Probes*, **10**:359-370.
- Trieselman B.A. et al., 1992. Transcriptionally active regions in the genome of the archaebacterium *Haloferax volcanii*. *J. Bact.*, **174** : 30-34.
- 30 Trieselmann, B. A., and R. L. Charlebois. 1992. Transcriptionally active regions in the genome of the archaebacterium *Haloferax volcanii*. *J. Bacteriol.* **174**:30-34.

Urdea M.S. et al., 1991, Nucleic Acids Symp. Ser., **24**:197-200.

Urdea M.S., 1988, Nucleic Acids Research, **11**: 4937-4957.

Van Soolingen D., 1993, J. Clin. Microbiol., **31** : 1987-1995.

- 5 Willets, N., and R. Skurray. 1987. Structure and function of the F-factor and mechanism of conjugation. In *Escherichia coli and Salmonella Typhimurium: Cellular and Molecular Biology* (F.C. Neidhardt, Ed) Vol.2 pp1110-1133, Am. Soc. Microbiol., Washington, DC.

- 10 Woo, S. S., J. Jiang, B. S. Gill, A. H. Paterson, and R. A. Wing. 1994. Construction and characterization of a bacterial artificial chromosome library of *Sorghum bicolor*. Nucleic Acids Res **22**:4922-4931.

Zimmer, R., and A. M. V. Gibbins. 1997. Construction and characterization of a large-fragment chicken bacterial artificial chromosome library. Genomics. **42**:217-226.

09673476-113000

M 21.06.00 AM 13.47

132

CLAIMS

1. A method for isolating a polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and that is absent or altered in the genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone belonging to a genomic DNA library of a given mycobacterium strain, said DNA library being cloned in a bacterial artificial chromosome (BAC) vector.
2. The method according to claim 1, wherein the BAC-based DNA library has been constructed from genomic DNA of *Mycobacterium tuberculosis*.
3. The method according to claim 2, wherein the BAC-based DNA library has been constructed from genomic DNA of *Mycobacterium tuberculosis* strain H37Rv.
4. The method according to claim 3, wherein the BAC-based DNA library has been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on November 19, 1997 under the accession number I-1945.
5. The method according to claim 1, wherein the BAC-based DNA library has been constructed from genomic DNA of *Mycobacterium bovis*.
6. The method according to claim 5, wherein the BAC-based DNA library has been constructed from the genomic DNA of *Mycobacterium bovis* BCG strain Pasteur.
7. The method according to claim 6, wherein said DNA library contains approximately 1600 clones and wherein the genomic DNA is cloned into a recombinant pBeloBAC11 vector with an average insert size of approximately 80 kb.
8. The method according to claim 6 or 7, wherein the at least one BAC-based DNA library has been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on June 30, 1998 under the accession number I-2049.

N 21.06.00

133

9. A method of isolating a polynucleotide of interest that is present in a genome of a first mycobacterium strain or that is expressed by the first mycobacterium strain and that is absent or altered in a genome of a second mycobacterium strain or that is not expressed by the second mycobacterium strain, said method comprising :

- a) providing at least one polynucleotide contained in a clone of a bacterial artificial chromosome (BAC) DNA library of the first mycobacterium strain;
- b) providing at least one genomic or cDNA polynucleotide from a second mycobacterium strain that is different from the first mycobacterium strain or at least one polynucleotide contained in a clone of a BAC DNA library prepared from the genome of the second mycobacterium strain;
- c) contacting under hybridizing conditions the polynucleotide of step a) with the polynucleotide of step b); and
- d) isolating the polynucleotide of step a) that has not formed a hybrid complex with the polynucleotide of step b).

10. The method of claim 9, wherein the polynucleotide contained in a clone of a BAC DNA library of the first or second mycobacterium strain is prepared by the following procedure :

- 1) digesting at least one recombinant BAC clone by an appropriate restriction endonuclease to yield a polynucleotide insert of interest; and
- 2) isolating the polynucleotide insert of interest.

11. A purified polynucleotide of interest that has been isolated according to the method of claim 9.

12. The purified polynucleotide of claim 11 which contains at least one Open Reading Frame (ORF).

13. The purified polynucleotide of claim 12, which is SEQ ID N0:1.

14. The purified polynucleotide of claim 12, wherein said polynucleotide is selected from the group consisting of :

21.06.00

134

- a) a polynucleotide comprising at least 8 consecutive nucleotides of SEQ ID N0:1;
- b) a polynucleotide having a sequence fully complementary to SEQ ID N0:1; and
- c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).
- 15 15. The purified polynucleotide of claim 14, which is SEQ ID N0:2.
16. The purified polynucleotide of claim 14, which is SEQ ID N0:3.
17. The purified polynucleotide of claim 12, wherein the ORF encodes all or part of a polypeptide involved in the pathogenicity of a mycobacterium strain.
- 10 18. The purified polynucleotide of claim 12, wherein the ORF encodes all or part of a Polymorphism Glycine Rich Sequence (PGRS).
19. The purified polynucleotide of claim 18, which is SEQ ID N0:4.
20. The purified polynucleotide of claim 18, which is selected from the group consisting of:
- 15 a) a polynucleotide comprising at least 8 consecutive nucleotides the of SEQ ID N0:5 ;
- b) a polynucleotide having a sequence that is fully complementary to SEQ ID N0:5 ;
- c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).
- 20 21. A pair of the purified polynucleotides as claimed in claim 11.
22. A *Mycobacterium tuberculosis* strain Rv37 genomic DNA library that has been deposited in the Collection Nationale de Cultures de Microorganismes under accession number I-1945, wherein said genomic DNA library comprises
- 25 recombinant bacterial artificial chromosome vectors.
23. A recombinant bacterial artificial chromosome (BAC) vector, which belongs to the genomic DNA library of claim 22.
24. The recombinant BAC vector of claim 23, which is selected from the group consisting of :



21.06.00

135

- Rv101; Rv102; Rv103; Rv104; Rv105; Rv106; Rv107; Rv108; Rv109; Rv110;  
 Rv110; Rv111; Rv112; Rv113; Rv114; Rv115; Rv116; Rv117; Rv118; Rv119;  
 Rv11; Rv120; Rv121; Rv122; Rv123; Rv124; Rv126; Rv127; Rv128; Rv129;  
 Rv130; Rv132; Rv134; Rv135; Rv136; Rv137; Rv138; Rv139; Rv13; Rv140;  
 5 Rv141; Rv142; Rv143; Rv144; Rv145; Rv146; Rv147; Rv148; Rv149; Rv14;  
 Rv150; Rv151; Rv152; Rv153; Rv154; Rv155; Rv156; Rv157; Rv159; Rv15;  
 Rv160; Rv161; Rv162; Rv163; Rv164; Rv165; Rv166; Rv167; Rv169; Rv16;  
 Rv170; Rv171; Rv172; Rv173; Rv174; Rv175; Rv176; Rv177; Rv178; Rv179;  
 Rv17; Rv180; Rv181; Rv182; Rv183; Rv184; Rv185; Rv186; Rv187; Rv188;  
 10 Rv18; Rv190; Rv191; Rv192; Rv193; Rv194; Rv195; Rv196; Rv19; Rv1; Rv201;  
 Rv204; Rv205; Rv207; Rv209; Rv20; Rv214; Rv215; Rv217; Rv218; Rv219;  
 Rv21; Rv220; Rv221; Rv222; Rv223; Rv224; Rv225; Rv226; Rv227; Rv228;  
 Rv229; Rv22; Rv230; Rv231; Rv232; Rv233; Rv234; Rv235; Rv237; Rv240;  
 Rv241; Rv243; Rv244; Rv245; Rv246; Rv247; Rv249; Rv24; Rv251; Rv252;  
 15 Rv253; Rv254; Rv255; Rv257; Rv258; Rv259; Rv25; Rv260; Rv261; Rv262;  
 Rv263; Rv264; Rv265; Rv266; Rv267; Rv268; Rv269; Rv26; Rv270; Rv271;  
 Rv272; Rv273; Rv274; Rv275; Rv276; Rv277; Rv278; Rv279; Rv27; Rv280;  
 Rv281; Rv282; Rv283; Rv284; Rv285; Rv286; Rv287; Rv288; Rv289; Rv28;  
 Rv290; Rv291; Rv292; Rv293; Rv294; Rv295; Rv296; Rv29; Rv2; Rv301;  
 20 Rv302; Rv303; Rv304; Rv306; Rv307; Rv308; Rv309; Rv30; Rv310; Rv311;  
 Rv312; Rv313; Rv314; Rv315; Rv316; Rv317; Rv318; Rv319; Rv31; Rv32;  
 Rv322; Rv327; Rv328; Rv329; Rv32; Rv330; Rv331; Rv333; Rv334; Rv335;  
 Rv336; Rv337; Rv338; Rv339; Rv33; Rv340; Rv341; Rv343; Rv344; Rv346;  
 Rv347; Rv348; Rv349; Rv34; Rv350; Rv351; Rv352; Rv353; Rv354; Rv355;  
 25 Rv356; Rv357; Rv358; Rv359; Rv35; Rv360; Rv361; Rv363; Rv364; Rv365;  
 Rv366; Rv367; Rv368; Rv369; Rv36; Rv370; Rv371; Rv373; Rv374; Rv375;  
 Rv376; Rv377; Rv378; Rv379; Rv37; Rv381; Rv382; Rv383; Rv384; Rv385;  
 Rv386; Rv387; Rv388; Rv389; Rv38; Rv390; Rv391; Rv392; Rv393; Rv396;  
 Rv39; Rv3; Rv40; Rv412; Rv413; Rv414; Rv415; Rv416; Rv417; Rv418; Rv419;

N 21.06.00

136

Rv41; Rv42; Rv43; Rv44; Rv45; Rv46; Rv47; Rv48; Rv49; Rv4; Rv50; Rv51; Rv52; Rv53; Rv54; Rv55; Rv56; Rv57; Rv58; Rv59; Rv5; Rv60; Rv61; Rv62; Rv63; Rv64; Rv65; Rv66; Rv67; Rv68; Rv69; Rv6; Rv70; Rv71; Rv72; Rv73; Rv74; Rv75; Rv76; Rv77; Rv78; Rv79; Rv7; Rv80; Rv81; Rv82; Rv83; Rv84; 5 Rv85; Rv86; Rv87; Rv88; Rv89; Rv8; Rv90; Rv91; Rv92; Rv94; Rv95; Rv96 and Rv9.

25. The recombinant BAC vector of claim 23, which is selected from the group consisting of:

Rv234; Rv351; Rv166; Rv35; Rv415; Rv404; Rv209; Rv272; Rv30; Rv228; 10 Rv233; Rb38; Rv280; Rv177; Rv48; Rv374; Rv151; Rv238; Rv156; Rv92; Rv3; Rv403; Rv322; Rv243; Rv330; Rv285; Rv233; Rv219; Rv416; Rv67; Rv222; Rv149; Rv279; Rv87; Rv273; Rv266; Rv25; Rv136; Rv414; Rv13; Rv289; Rv60; Rv104; Rv5; Rv165; Rv215; Rv329; Rv240; Rv19; Rv74; Rv411; Rv167; Rv56; Rv80; Rv164; Rv59; Rv313; Rv265; Rv308; Rv220; Rv258; Rv339; Rv121; 15 Rv419; Rv418; Rv45; Rv217; Rv134; Rv17; Rv103; Rv21; Rv22; Rv2; Rv270; Rv267; Rv174; Rv257; Rv44; Rv71; Rv7; Rv27; Rv191; Rv230; Rv128; Rv407; Rv106; Rv39; Rv255; Rv74; Rv355; Rv268; Rv58; Rv173; Rv264; Rv417; Rv401; Rv144; Rv302; Rv81; Rv163; Rv281; Rv221; Rv420; Rv175; Rv86; Rv412; Rv73; Rv269; Rv214; Rv287; Rv42 and Rv143.

20 26. A *Mycobacterium bovis* BCG strain Pasteur genomic DNA library, wherein said genomic DNA library comprises recombinant bacterial artificial chromosome vectors.

27. A *Mycobacterium bovis* BCG strain Pasteur genomic DNA library according to claim 26, wherein said DNA library contains approximatively 1600 25 clones and wherein the genomic DNA is cloned into a recombinant pBeloBAC11 vector with an average insert size of approximately 80 kb.

28. A *Mycobacterium bovis* BCG strain Pasteur genomic DNA library according to claim 26, that has been deposited in the Collection Nationale de

N 21.06.00

137

Cultures de Microorganismes (CNCM) on June 30, 1998 under the accession number I-2049.

29. A recombinant bacterial artificial chromosome (BAC) vector, which belongs to the genomic DNA library of claims 26 to 28.

5 30. A recombinant BAC vector according to claim 29, which is selected from the group consisting of:  
X0001; X0002; X0003; X0004; X0006; X0007; X0008; X0009; X0010; X0012;  
X0013; X0014; X0015; X0016; X0017; X0018; X0019; X0020; X0021 and  
X0175.

10 31. A method for detecting a mycobacterial nucleic acid in a biological sample comprising the steps of:

- a) contacting the recombinant BAC vector according to claim 23 or 29, or a purified polynucleotide according to claim 11 with the mycobacterial nucleic acid in the biological sample ; and  
15 b) detecting a hybrid nucleic acid molecule formed between said recombinant BAC vector or said purified polynucleotide and the mycobacterial nucleic acid in the biological sample.

32. The method of claim 31, further comprising before step a), making the mycobacterial nucleic acid in the biological sample available to a hybridization  
20 reaction.

33. A method for detecting mycobacterial nucleic acid in a biological sample comprising the steps of:  
a) contacting a first polynucleotide according to claim 11 that has been immobilized onto a substrate with the mycobacterial nucleic acid in the  
25 biological sample ; and  
b) contacting a hybrid nucleic acid molecule formed between said first polynucleotide and the mycobacterial nucleic acid in the biological sample with a second, labeled polynucleotide according to claim 11, wherein said

N 21.06.00

138

second polynucleotide and said first polynucleotide have non-overlapping sequences.

34. The method of claim 33, further comprising before step a), making the mycobacterial nucleic acid in the biological sample available to a hybridization  
5 reaction.

35. The method of claim 33 or 34, further comprising before step b), removing the mycobacterial nucleic acid that is not hybridized with the immobilized first polynucleotide.

36. A method for detecting mycobacterial nucleic acid in a biological  
10 sample comprising the steps of:

- a) contacting the mycobacterial nucleic acid in the biological sample with a pair of purified polynucleotides according to claim 21 ;
- b) amplifying said mycobacterial nucleic acid ; and
- c) detecting the amplified mycobacterial nucleic acid.

37. The method of claim 36, further comprising before step a), making the mycobacterial nucleic acid in the biological sample available to a hybridization  
15 reaction.

38. A kit for detecting a mycobacterium in a biological sample comprising:

- a) a recombinant BAC vector according to claim 23 or 29, or a purified  
20 polynucleotide according to claim 11 ; and
- b) reagents necessary to perform a nucleic acid hybridization reaction.

39. A kit for detecting a mycobacterium in a biological sample comprising:

- a) a recombinant BAC vector according to claim 23 or 29, or a first  
polynucleotide according to claim 11 that is immobilized onto a substrate ;
- 25 b) reagents necessary to perform a nucleic acid hybridization reaction ; and
- c) a second polynucleotide according to claim 11, wherein said second polynucleotide is radioactively or non-radioactively labeled, and wherein said second polynucleotide and said first polynucleotide have non-overlapping sequences.

N 21.06.00

139

40. A kit for detecting a mycobacterium in a biological sample comprising:
- a) a pair of purified polynucleotides according to claim 20 ; and
  - b) reagents necessary to perform a nucleic acid amplification reaction.

41. A method for detecting the presence of a genomic DNA, a cDNA or a mRNA of a mycobacterium in a biological sample, comprising the steps of:
- a) contacting the biological sample with a plurality of BAC vectors according to claim 23 or 29, or purified polynucleotides according to claim 11 that are immobilized on a substrate ; and
  - b) detecting the hybrid complexes formed.

42. A kit for detecting a genomic DNA, a cDNA or a mRNA of a mycobacterium in a biological sample, comprising:
- a) a substrate on which a plurality of BAC vectors according to claim 23 or 29, or purified polynucleotides according to claim 11 have been immobilized.

43. A method for detecting a polynucleotide of mycobacterial origin in a biological sample, said method comprising:
- a) aligning at least one polynucleotide contained in a recombinant BAC vector according to claim 23 or 29 on the surface of a substrate ;
  - b) contacting the polynucleotide in the biological sample with the substrate on which the polynucleotide of step a) has been aligned ; and
  - c) detecting a hybrid nucleic acid molecule formed between the polynucleotide in the biological sample and the aligned polynucleotide of step a).

44. A kit for detecting a polynucleotide of mycobacterial origin in a biological sample, comprising:
- a) a substrate on which at least one polynucleotide contained in a recombinant BAC vector according to claim 23 or 29 has been aligned.

45. The method of claim 10, wherein the procedure by which the polynucleotide contained in a clone of a BAC DNA library is prepared, further comprises amplifying the polynucleotide insert.

N 21.06.00

140

46. The method of claim 10, wherein the procedure by which the polynucleotide contained in a clone of a BAC DNA library is prepared, further comprises digesting the polynucleotide insert with at least one restriction endonuclease.

5        47. The method of claim 45, further comprising digesting the amplified polynucleotide insert with at least one restriction endonuclease.

48. The Polynucleotide of claim 17, wherein the mycobacterium strain is *Mycobacterium tuberculosis*.

49. The method of claim 36, wherein the amplified mycobacterial DNA is  
10 detected by gel electrophoresis or with a labeled polynucleotide according to claim 11.

50. The kit of claim 40, further comprising a polynucleotide according to claim 11.

51. The kit of claim 42, further comprising reagents necessary to perform a  
15 hybridization reaction.

52. A method for physically mapping a polynucleotide of mycobacterial origin in a biological sample, said method comprising:

- a) aligning at least one polynucleotide contained in a recombinant BAC vector according to claim 23 or 29 on the surface of a substrate;  
20 b) contacting the polynucleotide in the biological sample with the substrate on which the polynucleotide of step a) has been aligned under hybridizing conditions; and  
c) detecting the location of the hybridized polynucleotide from the biological sample.

25        53. The kit of claim 44, further comprising reagents necessary for labeling DNA and reagents necessary for performing a hybridization reaction.

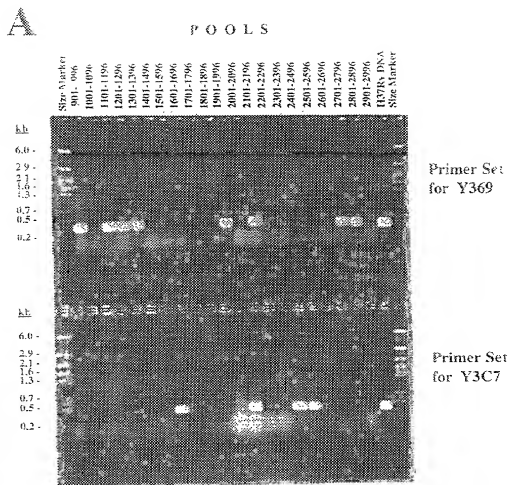


FIGURE 1A

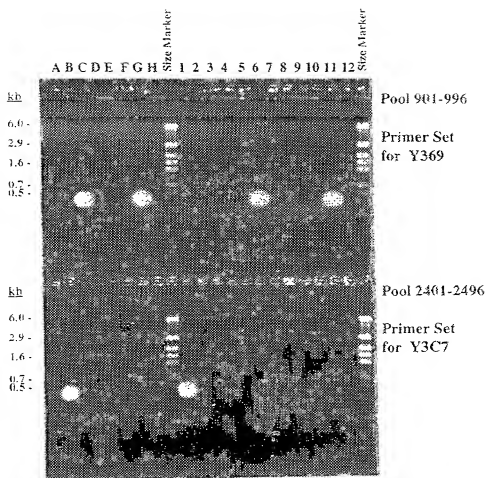
**B**

FIGURE 1B



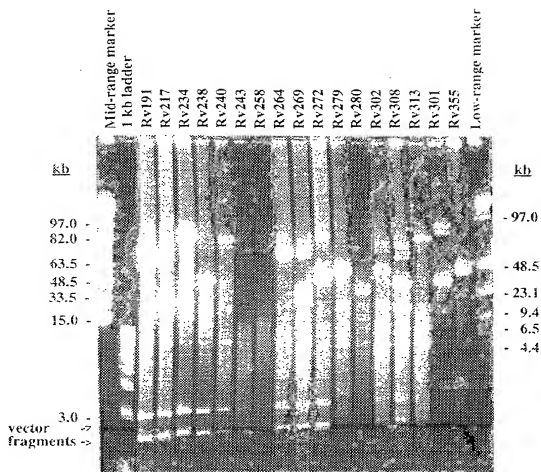


FIGURE 2

SUBSTITUTE SHEET (RULE 26)

FIGURE 3

A

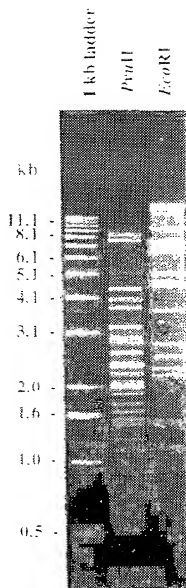


FIGURE 4A

B

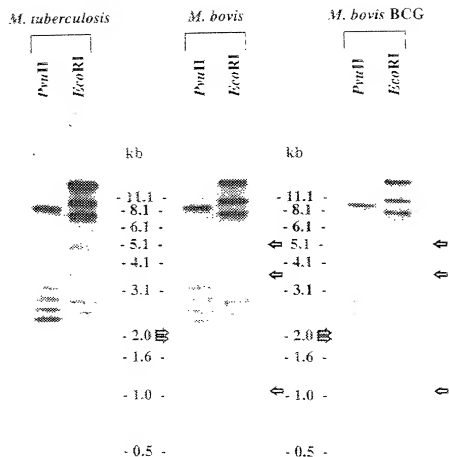


FIGURE 4B

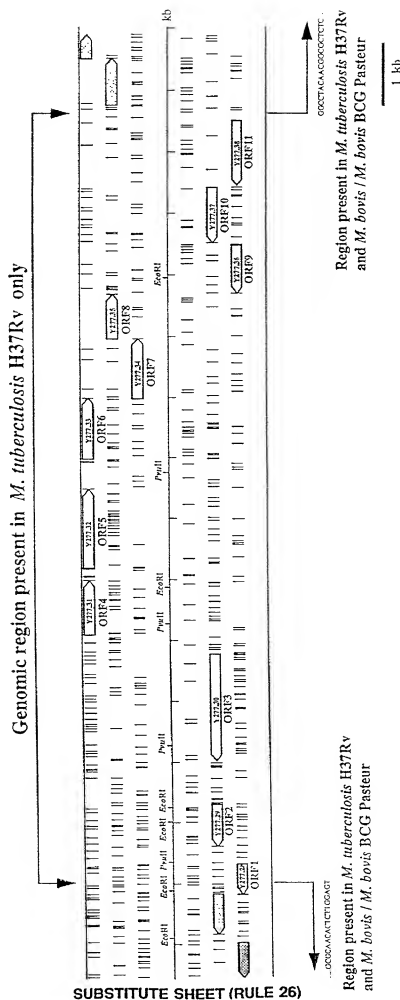


FIGURE 5

H37R+	PTOTLTGRPLIGHGTFGAVGSGATGAPGGWLLGDDGAGGSGAAGSGAPGGAGGAAGLWGT	837272
BCG	PTOTLTGRPLIGHGTFGAVGSGATGAPGGWLLGDDGAGGSGAAGSGAPGGAGGAAGLWGT	
H37R+	GGAGGAGGSSAGGCGAGGAGGAGGWLLOGDGAGGIGGASTYLTGCTGGGCGVGGIWFAGGGA	837453
BCG	-----GGAGGIGGASTYLTGCTGGGCGVGGIWFAGGGA	
H37R+	GGAGGTGLYGGDGGAGGAGCTGGLLAGLTCAGGGHGTGCLSTWGDGGYCGAGGNAGHLA	837633
BCG	GGAGGTGLYGGDGGAGGAGCTGGLLAGLTCAGGGHGTGCLSTWGDGGYCGAGGNAGHLA	
H37R+	GPGGAGGAGGDGEMLDTGDDGGAGGSAGLLTSGGAGGAGGFGTFLGGDGGAGGNAGLLLS	837813
BCG	GPGGAGGAGGDGEMLDTGDDGGAGGSAGLLTSGGAGGAGGFGTFLGGDGGAGGNAGLLLS	
H37R+	SGGAGGFGGTAGCGVGGAGGNAGWLGF-----	837897
BCG	SGGAGGFGGTAGCGVGGAGGNAGWLGF-----	
H37R+	-----GGAGCGGGSAGLITGTCGNGGNGGTGANAGSPCTGGAGCLLTCQNLGCLP	83804
BCG	GVFGGAALSYGDTGGAGGCGGGSAGLITGTGCGNGGNGGTGANAGSPCTGGAGCLLTCQNLGCLP	

FIGURE 6

pBeloBAC11

GGGGGCGGAA GGGGTTTCGCG TCAGCGGGTG TTGGCGGGTG TCGGGGCTGG

NoI restriction site

CTTAACTATG CGGCATCAGA GCAGATTGTA CTGAGAGTGC ACCATATGCG

GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC ATCAGGCGCC

ATTCGCCATT CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC

TCTTCGCTAT TACGCCAGCT GGCAGAAAGGG GGATGTGCTGCAAGGGGATT

primer T7-BAC1

AAGTTGGGTA ACGCCAGGGT TTTCCAGTC ACGACGTTGT AAAACGACGG

CCAGTGAATTGTAAATACGAC TCAGTATAGGCGCAATTCGA GCTCGGTACC

T7-promoter sequence

CGGGGATCCTCTAGAGTCGACCTGCAGGCA TGCAGGCTTG AGTATTCAT

primer T7-Belo2

HindIII cloning site

SP6-promoter

AGTGTGACCTAAATAGCTTGCGCTAATCATGGTCATAGCTGTCTCTGTG

sequence (complementary strand)

primer SP6-Mid (complementary strand)

TGAAATTGTT ATCCGCTCAC AATCCACAC AACATACGAG CCGGAAGCAT

AAAGTGTAAG GCCTGGGCTGCCTAATGAGTGAAGT ACATTAATTG

primer SP6-BAC1 (complementary strand)

CGTTGCGCTC ACTGCCCGCT TTCCAGTCGG GAAACCTGTC GTGCCAGCTG

CATTAATGAA TCGGCCAACG CGAACCCCTT GGGGCGGC GGGCCGTCGA

NoI restriction site

FIGURE 7

## DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that: my residence, post office address and citizenship are as stated below next to my name; I believe I am the original, first, and sole inventor (if only one name is listed below) or an original, first, and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled: **A method for isolating a polynucleotide of interest from the genome of a mycobacterium using a BAC-based DNA library. Application to the detection of mycobacteria**

the specification of which is attached and/or was filed on April 16, 1999 as United States Application Serial No. \_\_\_\_\_ or PCT International Application No. PCT/IB99/00740 and was amended on \_\_\_\_\_ (if applicable)

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above. I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR § 1.56.

I hereby claim foreign priority benefits under 35 U.S.C. § 119(a)-(d) or § 365(b) of any foreign application(s) for patent or inventor's certificate or § 365(a) of any PCT International application(s) designating at least one country other than the United States, listed below and have also identified below, any foreign application(s) for patent or inventor's certificate, or any PCT International application(s) having a filing date before that of the application(s) of which priority is claimed:

Country	Application Number	Date of Filing	Priority Claimed Under 35 U.S.C. 119
US	09/060 756	16/04/1998	<input type="checkbox"/> YES <input type="checkbox"/> NO
			<input type="checkbox"/> YES <input type="checkbox"/> NO

I hereby claim the benefit under 35 U.S.C. § 119(e) of any United States provisional application(s) listed below:

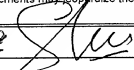
Application Number	Date of Filing

I hereby claim the benefit under 35 U.S.C. § 120 of any United States application(s) or § 365(c) of any PCT International application(s) designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application(s) in the manner provided by the first paragraph of 35 U.S.C. § 112, I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR § 1.56 which became available between the filing date of the prior application(s) and the national or PCT International filing date of this application.

Application Number	Date of Filing	Status (Patented, Pending, Abandoned)

I hereby appoint the following attorney and/or agent(s) to prosecute this application and transact all business in the Patent and Trademark Office connected therewith: FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER, L.L.P., Douglas B. Henderson, Reg. No. 20,291; Ford F. Farabow, Jr., Reg. No. 20,630; Arthur S. Garrett, Reg. No. 20,338; Donald R. Dunner, Reg. No. 19,023; Brian G. Brunsvold, Reg. No. 22,593; Tipton D. Jennings, IV, Reg. No. 20,645; Jerry D. Voght, Reg. No. 23,020; Laurence R. Hetter, Reg. No. 20,627; Kenneth E. Payne, Reg. No. 23,028; Herbert H. Mintz, Reg. No. 26,694; C. Larry O'Rourke, Reg. No. 26,014; Albert J. Santorelli, Reg. No. 22,640; Michael C. Elmer, Reg. No. 25,857; Richard H. Smith, Reg. No. 20,608; Stephen L. Peterson, Reg. No. 26,326; John M. Romary, Reg. No. 26,331; Bruce C. Zotter, Reg. No. 27,680; Dennis P. O'Reilly, Reg. No. 27,932; Allen M. Sokal, Reg. No. 26,695; Robert D. Bajefsky, Reg. No. 25,387; Richard L. Stroup, Reg. No. 28,478; David W. Hill, Reg. No. 28,220; Thomas L. Irving, Reg. No. 28,619; Charles E. Lipsey, Reg. No. 28,165; Thomas W. Winland, Reg. No. 27,605; Basil J. Lewis, Reg. No. 28,818; Martin I. Fuchs, Reg. No. 28,508; E. Robert Yoches, Reg. No. 30,120; Barry W. Graham, Reg. No. 29,924; Susan Haberman Griffen, Reg. No. 30,900; Richard B. Racine, Reg. No. 30,419; Thomas H. Jenkins, Reg. No. 30,854; Robert E. Converse, Jr., Reg. No. 27,432; Clair X. Mullen, Jr., Reg. No. 20,948; Christopher P. Foley, Reg. No. 31,354; John C. Paul, Reg. No. 30,413; Roger D. Taylor, Reg. No. 28,992; David M. Kelly, Reg. No. 32,883; Kenneth J. Meyers, Reg. No. 25,146; Carol P. Einaudi, Reg. No. 32,220; Walter Y. Boyd, Jr., Reg. No. 31,738; Steven M. Anzalone, Reg. No. 32,085; Jean B. Fordis, Reg. No. 32,984; Barbara C. McCurdy, Reg. No. 32,120; James K. Hammond, Reg. No. 31,664; Richard V. Burghjian, Reg. No. 31,744; J. Michael Jakes, Reg. No. 32,924; Dirk D. Thomas, Reg. No. 32,600; Thomas W. Banks, Reg. No. 32,719; Christopher P. Isaac, Reg. No. 32,616; Bryan C. Diner, Reg. No. 32,409; M. Paul Barker, Reg. No. 32,013; Andrew Chanho Sonu, Reg. No. 33,457; David S. Forman, Reg. No. 33,694; Vincent P. Kovalick, Reg. No. 32,867; James W. Edmondson, Reg. No. 33,871; Michael R. McGurk, Reg. No. 32,045; Joann M. Neth, Reg. No. 36,363; Gerson S. Panitch, Reg. No. 33,754; Cheni M. Taylor, Reg. No. 33,216; Charles E. Van Horn, Reg. No. 40,266; and Linda A. Vadtler, Reg. No. 33,218; and \_\_\_\_\_ Please address all correspondence to FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER, L.L.P., 1300 I Street, N.W., Washington, D.C. 20005. Telephone No. (202) 408-4000.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Full Name of First Inventor <u>COLE Stewart</u>	Inventor's Signature 	Date <u>Nov. 3, 2000</u>
Residence <u>92140 CLAMART, FRANCE</u>	Citizenship <u>GB</u>	
Post Office Address <u>23 bis rue Cécile Dinant</u>		

Listing of Inventors Continued on Page 2 hereof. ☐ Yes ☐ No



Listing of Inventors Continued From Page 1 hereof.

Full Name of Second Inventor <b>BUCHRIESER-BROSCH Roland</b> 2-00	Inventor's Signature <i>[Signature]</i>	Date <b>Nov. 3, 2000</b>
Residence <b>75014 PARIS, FRANCE</b>	New address: <b>11 rue de l'Amiral Mouchez - 75013 Paris / France</b>	Citizenship <b>AT</b>
Post Office Address <b>7 F boulevard Jourdan</b> FR		
Full Name of Third Inventor <b>GORDON Stephen</b> 3-00	Inventor's Signature <i>[Signature]</i>	Date <b>Nov. 3, 2000</b>
Residence <b>75015 PARIS, FRANCE</b>	New address: <b>48 Broadacres, Guilford Surrey GU3 3BB / United Kingdom</b> SS GB	Citizenship <b>IE</b>
Post Office Address <b>82 rue Dutot</b>		
Full Name of Fourth Inventor <b>BILLAULT Alain</b> 4-00	Inventor's Signature <i>[Signature]</i>	Date <b>Nov. 3, 2000</b>
Residence <b>77680 ROISSY EN BRIE, FRANCE</b> FR		Citizenship <b>FR</b>
Post Office Address		
Full Name of Fifth Inventor	Inventor's Signature	Date
Residence		Citizenship
Post Office Address		
Full Name of Sixth Inventor	Inventor's Signature	Date
Residence		Citizenship
Post Office Address		
Full Name of Seventh Inventor	Inventor's Signature	Date
Residence		Citizenship
Post Office Address		
Full Name of Eighth Inventor	Inventor's Signature	Date
Residence		Citizenship
Post Office Address		
Full Name of Ninth Inventor	Inventor's Signature	Date
Residence		Citizenship
Post Office Address		
Full Name of Tenth Inventor	Inventor's Signature	Date
Residence		Citizenship
Post Office Address		

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

- (A) NAME: INSTITUT PASTEUR
- (B) STREET: 28 RUE DU DOCTEUR ROUX
- (C) CITY: PARIS CEDEX 15
- (E) COUNTRY: FRANCE
- (F) POSTAL CODE (ZIP): 75724

(ii) TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA LIBRARY. APPLICATION TO THE DETECTION OF MYCOBACTERIA.

(iii) NUMBER OF SEQUENCES: 5

## (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ACCTGCGCTT GCAGAGATCA AATAGGGCGC ATGGGTGAGC ATAGTACAGG TCGTCGCGCA	60
TCTTTGATGC ATCGGAATAA GATGTCAGGC AATTAAAAGA GAAGCCACGG CGACTCGCGG	120
CATTTCAGCAT GTCGAGCGTC GCTTCGATGT GAGCGCACCA TTCCGTGTCC AACGATTTCA	180
GACGAACATT GAATATTCCA CTCGCGACGC TATAGTCCGC CTCCCGATCT ATGCGCGCCG	240
CGCAGATGAA GTCTGCGTTC GCCCGACCTT CGAAACGTAG TCGGCGCCGCG CGCACCATTT	300
CGGGGGAGAC GTCGATGCCG GTGTAATCAG TTTTGAAGCC ACGCGCATCT AGGTAGTCCA	360
GTAGAGCCCC ATAGCCACAG CCTAGATCGT TGATCGAAAA TGGGTCCGCC GCATTGACAA	420
TGCGCACCAAG CTGGTCAAAG CGCAACGCCT GCCCGGCTTC GCGGTTCCAA TCGAGCGCCG	480
GCGGGTGCCG TGTGCTTCGA GTTTCGATGC GTAGTAACGG GCCACGTGAG CGAGCATGGT	540

CGTTGCGTCT TCCGCCATGA AGCTGCCTCA CGATTGTGT GTGTGGGCGT CGGTGCGTGG 600

GTCCGAGACT ATACCTTCAA CAGTTGCATG CCGAGGCTGC GCGGGGCAAT GACCCAAAAA 660

CCCGCCGGCA CGGTTCCGCG AGCAAGGAAG CGTGAGACG ATAGATAATT TCACTGGCGA 720

CAGTACCTCA AATAGTCCGG AGCCTCGGCT CCGACGTTAA AGAGCAGATC CAGAATCGAC 780

ACGGCGGGCT CGAACCTCC CCACAATTGC TTATAATCGC GGTAGCCGTC ATAATCGAAC 840

CAAGTTACCC GGATGCTAAG TTCGTCGAAC ACGCGCTCAT CGACATACGA ACGGGCTGAG 900

GGCCAGAGA CATATTCGGT CGTCGCGGCC TGTGGCAGA GGTGGCCAG TCTCTCGGTC 960

TTGCCGTCG CTAATTCGTA GTCCACGAA TTTGCCAGTC CGTGCTGAT ACCGAGATAA 1020

CTGCAATCG CATTCAATAG ACGCCTGTTG AGTAAGGAAA GATTCTGTG CTGTTCTTCG 1080

AGGTAAATCG GCGCGAGCCA GTCAGCGATC TCCGCAAAAT GAGCGGCCG GCTGTAGTTG 1140

AATTCTAGTG CCCGCCAGTG CGCTTTGCC CAATCGGTGC CGTCGATCAG CGTCTCACGT 1200

ATCTTTTGT GAAACGTC CTTCACCTGG ACGGGAACAG TTATCCACTG TAACCCCTGG 1260

CTCGTTTTGA TCCGATTCT GTTTCGCCAA TCACGCTTGG TATATTGAT GTCATCATAG 1320

ATGATGAATT CATCGACGAA TGCAATCAGG TCAAAATATC CTCGCCAAG TATGTAATTT 1380

GATTGAACAA TCGCGACTTT CTTCACGCG GTGCTCCAA TTTAGAATAA CAAATACGTC 1440

GCGCCGCGA CAGCTCCGCT GGAGCGAGTT CAAGCGATTC TCGACATAT TCAATATGGT 1500

GCTCGGGAAG GCCAGGATGG GCCGCGACCC GGGGCGTCCG GTGCGCGATG AACGTCGCAT 1560

CGTCTCTGT GAGATAATTG CATCCGATCA TATAGGGCTG GCTCGGCTA GGTGTCTGGC 1620

AAAAAGATAT CCGCGCCGAT CGGTTTCTGG TTTGTCTTG ATGATCAAA CCGCTTCCGT 1680

TCACGAGATC GATTCTGTT CTTCCTCCAG CGTCGCGATG TCGATAGTG TCGCGCTTGG 1740

TTCTGATCCG CACTACGCG CGGCGAGAAC CTCGCCACCG AATCGGGATT GGGGGGAGGA 1800

TACCACTCG TCGAGGCCG TCACCGGCT TCTAGCGGTG TGACCATCAG TGTTTGACGG 1860

GCCCTATCCC GGTATGGCG ACCACGGGAT CGGCGCGCTT CCGGTTGCTG GCGTGGTACC 1920

TCGTTGTGGC GCCGTGGTCC ATGTCGATTG AGTGGTGA TCAAGTAAA CCGTTGCGCG 1980

CCATGTTCTG TAGGCACTGG TTCGGTTGT GGTAGGCTG CACGTTGGC AGGTTACCAA 2040

CCACTGAGCC CCTGGGCGA TGTGAGCTG GACTCCGCT ATGGGGTGA ATTTTGGCAG 2100

ATTGGGCGG GTCCCGTGG TAGGACTCC TCAACCGGAT TGGGTAAGCA TGAGSTGGT 2160

CTGGACGCG TGTCTGGT GCTCTCCGA GTAGGCCCTG TGTACTGTC ATGTGGGCGA 2220

0067476.1.1000

GCGGGTTTGC GCGCGTAGGA GACGATGATT ACTACGCACG TGACCAACCA CAAGAACGGT 2280  
 GCCCATGTCA CCGTSGTGAA AACGAGTGGC GTGGTACCGA CTACCCCTTT GGCTCCCAGC 2340  
 TGTCCATAGA GCGGCACGTA GAACGGCTGG CCCGGGACCG CGACGTTGAC GATGCTCAGC 2400  
 GCCACGGCCA AACTCACGCA GACGCCGACC GCGCGCGCGG GGTCTCCATG GGCTGCGAGT 2460  
 TGGTCGAATA TCCAGCACC AGGAGGCCCG TTGGGGTCTC GGGCTACCAG TGCAGCGATT 2520  
 GGCAAGACGA AAACGAGATA GTAGAAGGCG ACGTCCGCGG GGGAGAAGGT GCGGTGGCG 2580  
 AGCAACACAA TCCCCACCAT GACAGGCGGG ATACGGCGTC CGAGCGCCAG CACGCGGACC 2640  
 ACGACTATGA CTAGGACAGC AAACCCGATC TCGGTTGCGG GACCACTGAG GAAACCTCT 2700  
 GGGATCTTGC CCGATTGATA GTTCTTGATG CTATCGGGGA TCAGCAGGAG TGCTTGCCA 2760  
 AAGGACACGT TCCGCGGGTC TCGAAGCCCT CGAACGAAAC TATTGAACCT GATGATGCCG 2820  
 TGGATCGACT GTGCGATCGT CCCCGGGAAG CCTCGTGGCC ACAACAGAAA GGTCTGCGATA 2880  
 TTGGACACCA CCACGCGGT GATCCCGATA CCAGCCCAAC GCCATTGTGCG AGCCGCCAAC 2940  
 AACCCACGC CGAGAACGAC GAACTGCGGC TTTACCAGGA CGGCCAAGAT CACCGTGATG 3000  
 GTGGCGAGGC CCCACGCGTG TCGGGACAAC GCCACGAAGT AAGCCAGCGC GATCGGTACC 3060  
 ACGAACCCCTG TCGAGTTGCC TCGATCGATG ACCCCCCACG CCGGGATGGC CGCGGCGCCC 3120  
 AGTGTCACGA AGATGACCAC TCGCTCCAGA CCACGTGCCC CCCGGGCCCG CCAGATGGCG 3180  
 GGAGATATGA CCGCCATCGT TAGGGCGACC AGGTAACAGA TCAGCCCCAA GCGCGGCGCA 3240  
 CCCAGCCAAT GGTGCGGTAG TCGAAAATC GCATACGGTA TCGGGGCGGG GGCCCATGCA 3300  
 GCAACCGCGG TCGGCTGGTA ATCGCGGGT AGCGAGATCA GGTAGTCCGC GGGATTGGGT 3360  
 TGAATCCCGG CGCGCGCGAC CATGGCGTAG TCGTGAAGC AGTGCCGACC GATATTCTATG 3420  
 CCCCAATCAA GCCAACAGTC CCCAGGGACT ACCAAAAGAG TGGAAAAGAC GTCACCCGCG 3480  
 TACCACTGAC TGAGGGCGTA CGCCGTCGCC GCCGAAATCA CGACGCCAG CAGGATGGTG 3540  
 CCGAGCATGA GGGTGCGCTC GGATTGGGAG COGATCGCCC AGAGCCGCTC CCGGCTCGCG 3600  
 GTCACGGCAC CGCGCAACAC CTCGGGGGT CGCTTCTATCT GGATTCTCTCT CGGTCTTGCG 3660  
 CGAAACGGTA GCAGAGCGCC ATGGTTGCCA ACGCGTTCGC CGGCAGTCT AGACCGGATC 3720  
 TTCTCTGTGG CAACCGACAA CAGGACGTCG TTGCCGAAAG GCGCTGGGC ACCGACATCT 3780  
 AGGATGAACC CACAGCCACG CCCCGACGTT ATGCCATGGC GAAGAGCGAC CGGCAGGAGC 3840  
 GGAACCCAG TGAAGCGAGC GCTCATCACC GGAATCACAG GACCGGACGG CTCGTATCTC 3900  
 GCTAAGCTCC CGCTGAAGG ATATGTGGCC GCTGGTAGCC CGGCCGAGGT CTATTCTGCG 3960

TGGGCGACAC GGAATTATCG CGAATTGTAT GGGTTGCTCG CGGTCAACAG CATCTGGTTC 4020  
 AATCACGAAT CACCGCGTCA CGGCGAGACA TTCATGACTC GTAATCTCTG ACCATATCGC 4080  
 GGTCGGCAAC GAGGCGCTGA TCGATGCGCA GACGCTGATG CGCCGGCCCA CCCGGATAGG 4140  
 TATCAGTATT GGGGCGTTCC GGCACGCTA CGAGGCGTGA TCGACCGCGC AATGGGTGTT 4200  
 TCGCTGAGT AATAATCTGA ACCGTGTGAA CGCATGCATG GATGGATTCC TTGCCCGTAT 4260  
 CCGCTCATAT GTTGATGCGC ACGCGCCAGA ATTGCGTTCA CTGTTCCGATA CGATGGCGGC 4320  
 CGAGGCCCGA TTTGCACGCG ACTGGCTGTC CGAGGACCTC GCGCGGTTGC CTGTCGGTGC 4380  
 AGCATTGCTG GAAGTGGGCG GGGGGGTACT TCTGCTCAGC TGTCAACTGG CGGCGGAGGG 4440  
 ATTTGACATC ACCGCCATCG AGCCGACGGG TGAAGGTTT GGCAAGTTCA GACAGCTTGG 4500  
 CGACATCGTG CTGGAATTGG CTGCAGCAGC ACCCACCATC GCGCCATGCA AGGCGGAAGA 4560  
 CTTTATTTCG GAGAAGCGGT TCGACTTCGC CTTCTCGCTG AATGTGATGG AGCACATCGA 4620  
 CCTTCCGGAT GAGGCAGTCA GCGGGGTATC GGAAGTGCTG AAACCGGGGG CCAGTTACCA 4680  
 CTTCTGTGTC CCGAATTACG TATTCCCGTA CGAACCGCAT TTCAATATCC CAACATTCTT 4740  
 CACCAAAGAG CTGACATGCC GGGTGATGCG ACATCGCATC GAGGGCAATA CGGCATGGA 4800  
 TGACCCGAAG GAGAGTCTGC GTTCGCTCAA CTGGATTACG GTTCCCAAGG TGAACGCTT 4860  
 TGCGGCGAAG GATGCGAGCG TGACCTTGC GCTCCACCGT GCAATGTTGG TATGGATGCT 4920  
 GGAACGCGCG CTGACGGATA AGGAATTGCG TGGTCGCGG GCACAATGGA TGTCGCTGC 4980  
 TATTCGCTCG GCGGTGAAAT TCGTGTGCA TCATCTGGCA GGTATGTTC CCGCTACGCT 5040  
 GCAGCCCATC ATGGATGTGC GGCTAACGAA GAGGTAATGA CATGGCGCAA GCGACATCGG 5100  
 GCATTGCGCG GGCACCTTCG CAACCTGCTG TGTATGAGGC GTATCAGCGG ATTGCGGGCG 5160  
 CTAAAAGCGG GCTTGCGTGG ATCACAACCG ACCCATCCA GTCGTTGCCA GGCATGCGTA 5220  
 CTCTCGACCT CGGTGCTGCG CCAGCGGTGA TACACAGCTC CCCGCCAGTG GACGTGACAT 5280  
 GTACGAGAGA CGGCATGAGC GCGGAATGTG CGACCGTGCC GTCGAGATGA CCGACGTCGG 5340  
 CGCTACGGCA GCGCCACCGG GACCTATCGC GCGGGGCGAG GTCGCTCGGG TCGGCGCGGC 5400  
 GACCGCGTTG GCGGTTGCCT GCGTCTACAC GGTCTATCTAT CTGGCGGCCC GCGACCTACC 5460  
 CCCGCGTTGT TTTTCGATAT TCGCGGTGTT TTGGGGGGCG CTCGGCATTG CCACCGCGCG 5520  
 CACCCACGGC CTCCTGCAAG AAACGACCCG CGAGGTCGCG TGGGTGCGCT CCACCCAAAT 5580  
 AGTTGCGGGC CATCGTACCC ATCCGCTGCG GGTGGCCGGG ATGATTGGCA CCGTCGCGGC 5640

CGTCGTAATT GCGGGTAGCT CACCGCTGTG GAGCCGACAG CTATTCGTCG AGGGGCGCTG 5700  
 GCTGTCCGTG GGGCTACTCA GCGTTGGGGT GGCCGGGTTC TGCGCGCAGG CGACCCTGCT 5760  
 GGGCGCGCTG GCCGGCGTGG ACCGGTGGAC ACAGTACGGG TCACTGATGG TGACCAGCGC 5820  
 GGTCAATCCG TTGGCGGTGG CCGCGGCAGC GGTGTGTGATC GGATGGGGTG TGCCCGGGTA 5880  
 CTTGTGGGCC GCCACCGCGG GAGCGGTGGC GTGGCTGCTC ATGCTGATGG CCTCGCCAC 5940  
 CGCGCGCAGC GCGGCCAGCC TGCTGACGCC CGGGGAATC GCCACGTTCT TGCGCGGTGC 6000  
 CGCTCATTCG ATAACCGCCG CCGGTGCCAG CGCGATTCTG GTAATGGGTT TCCAGTGGTT 6060  
 GCTCAAAGTG ACCTCCGACC AGTTAGGGGC AAAGGGCGGA GCGGTCATCC TGGCTGTGAC 6120  
 CTTGACCGGT GCGCCGCTTC TGGTCCCACT GAGCGCGATG CAAGGCAACC TGATCGCGCA 6180  
 TTTCGTCGAC CGGCGCACCC AACGGCTTCG GCGCTGTATC GCACCGGCGC TGGTCGTCGG 6240  
 CGGCATCGGT GCGGTCCGGA TGTTGGCCGC AGGGCTTACC GGTCCCTGGT TGCTGCGTGT 6300  
 TGGATTGCGC CCCGACTACC AAATGCGCGG GCGCTGTGCTG GCCTGCTTGA CGCGACGGCG 6360  
 GGTAGCTATC GCCATGCTGA CGTGACCGG CGCCGCCGCG GTCGCGGCGG CACTGCACCG 6420  
 GCGGTATTGG CTGGGCTGGG TCAGCGCGAC GGTGGCGTCG ACGCTGTTGC TGCTGCTGCC 6480  
 GATGCCGCTG GAGACGCGCA CCGTGATCGC GCTGTGTTC GGTCCAACGG TGGGAATCGC 6540  
 CATCCATGTG GCCGCGTTGG CGCGGCGACC CGACTGATTT GTGCCCAGG TCGACAAATC 6600  
 ACGCCGCTCT GTCAGTGAGC ACTCCGTCCT CGGGTCCGAT CCTTCCAGGA GAGCTTGCAA 6660  
 CCTGATTGG CTCAAATTGG TGCGCACCGA GGGTCGGGCA CATCGTAGGG TCGCAACAGT 6720  
 CACATGTGTC ACTGCACCGG GCGACACCGG ATGTCCCGGC TCTCAGCGAC AGCTGTCTGA 6780  
 CCTGTGGTTT TGTTCCCAAG TTGGTCGTGG CTGTGCGGGA TTGGAGGTGG CGTGGGGGTC 6840  
 GCGTCGTATG GATTCTCCTC CTCGGTTCGG CGCGAAACGG CGCAGGCGC AATGTCACCC 6900  
 AACTTGGCCG CGGTGGAGTC TAGCCTCACA TTTTCTGGT CGCCCCGAC AACCAGGAGG 6960  
 TCGCTGCAGA ACGGGCGTTC CCTACCCACA TCTACTATGA AGCGACAGCG GCGCCCCGCT 7020  
 GTGATGGCTG AGCATGACCG ACAGAGGCGG GAAGACAGTG AAGCGAGCGC TCATCACCAG 7080  
 AATCACCGGC CAGGACGGCT CGTATCTCGC CGAACTGCTG CTGGCCAAGG GGTATGAGGT 7140  
 TCACGGGCTC ATCCGGCGCG CTTGACGTTT CAACACCTCG CGGATCGATC ACCTCTACGT 7200  
 CGACCCGCGC CAACCGGGCG CGCGGCTGTT TCTGCACTAT GGTGACCTGA TCGACGGAAC 7260  
 CCGGTGGGTG ACCCTGCTGA GCACCATCGA ACCGACGAG GTGTACAACC TGGCGGCGCA 7320  
 GTCACACGTG CCGGTGAGCT TCGACGAACC CGTGACACCC GGTGACACCA CCGCATGGG 7380

ATCCATGCGA CTGCTGGAAG CCGTTCGGCT CTCTCGGGTG CACTGCCGCT TCTATCAGGC 7440  
 GTCCCTCGTCG GAGATGTTCTG GCGCCTCGCC GCCACCGCAG AACGAGCTGA CGCCGTTCTA 7500  
 CCGCGGGTCA CCGTATGGCG CCGCCAAGGT CTATTCTGTAC TGGGCGACCC GCAATTATCG 7560  
 CGAAGCGTAC GGATTGTTCTG CCGTTAACGG CATCTTGTTC AATCACGAAT CACCCGCGCG 7620  
 CGGTGAGACG TTCGTGACCC GAAAGATCAC CAGGGCCGTG GCACGCATCA AGGCCGGTAT 7680  
 CCAGTCCGAG GTCTATATGG GCAATCTGGA TGCCTCCCG GACTGGGGGT ACGCGCCCGA 7740  
 ATACGTGCAA GGCATGTGGC GGATGCTGCA GACCACGAG CCCGACGACT TCGTTTTGGC 7800  
 GACCGGGCGC GGTTCACCG TGCCTGAGTT CCGCGGGGCC GCGTTCGAGC ATGCCGGTTC 7860  
 GGACTGGCAG CAGTACGTGA AATTCGACCA ACGCTATCTG CGGCCACCG AGGTGGATTC 7920  
 GCTGATCGGC GACGCGACCA AGGCTGCCGA ATTGCTGGGC TGGAGGGCTT CGGTGCACAC 7980  
 TGACGAGTTG GCTCGGATCA TGGTCGACGC GGACATGGCG GCGCTGGAGT CGGAAGGCAA 8040  
 GCCGTGGATC GACAAGCCGA TGATCGCCGG CCGGACATGA ACGCGCACAC CTCGGTCGSC 8100  
 CCGCTTGACC GCGCGGCCCG GGTCTACATC GCCGGGCATC GCGGCTTGGT CGGGTCCGCG 8160  
 CTGCTACGCA CGTTTGCGGG CCGGGGGTTC ACCAACCTGC TGGTGCGGTC ACGCGCCGAG 8220  
 CTGTGATCTGA CGGATCGGC CCGGACGTTT GACTTCGTTT TCGAGTCGAG GCCCGAGTTC 8280  
 GTCATCGACG CGGCGGCCCG GGTGCGCGGC ATCCTGGCCA ACGACACCTA CCCGGCCGAT 8340  
 TTCTGTCGCG AAAACCTCCA GATCCAGTTC AACCTGCTGG ATGCCGCCGT GGCAGCGCGG 8400  
 GTGCCCGCGC TGCTGTTCTT GGGCTCGTCG TGCATCTACC CGAAACTCGC CCCGACGCG 8460  
 ATCCCGGAGA GCGCGCTGCT CACCGGTCCG TTGGAGCCGA CCAACGACGC GTACCGGATC 8520  
 GCCAAAATCG CCGGCATCCT TGCCTGCCAG GCGGTGCGCC GCCAACATGG CCTGCCCTGG 8580  
 ATCTCGGCGA TGCCACCAA CCTGTACGGG CCAGGCGACA ACTTTTCGCC GTCCGCTCG 8640  
 CATCTGCTCG CGGCACTCAT CCGCGCTAT GACGAGGCCA AAGCCAGTGG CGCGCCCAAC 8700  
 GTGACCAACT GGGGCACCG CACGCCCGCA CCGGAGTTGC TGCACGTCGA CGACCTGGCG 8760  
 AGCGCATGCC TGTATCTGCT GGAACATTTC GACGGGCCGA CCCATGTCAA CGTGGGAACC 8820  
 GGCATCGACC ACACCATCGG CGAGATCGCC GAGATGGTGG CCTCGGCGGT AGGCTATAGC 8880  
 GGCAGAAACC GCTGGGATCC AAGCAAACCG GACGGAACAC CACGCAAACT GCTGGATGTT 8940  
 TCGGTGCTAC GGGAGGCGGG ATGGCGGCCT TCGATCGCGC TCGCGCAGCG CATCGAGGCG 9000  
 ACGGTGGCGT GGTATCGCGA GCACGCGGGA ACGGTTCCGGC AATGAGGCTG GCCCGTCGCG 9060

09573476.113000

CTCGGAACAT	CTTGCGTGC	AACGGCATCG	AGGTGTGCGG	CTACTTTGCC	GAACTGGACT	9120
GGGAACGCAA	TTTCTTGCGC	CAACTGCAAT	CGCATCGGT	CAGTGCCGTG	CTCGATGTCG	9180
GGGCCAATTC	GGGGCAGTAC	GCCAGGGGTC	TGCGCGGGCG	GGGCTTGCGG	GGCCGCATCG	9240
TCTCGTTTCA	GCCGCTGCC	GGGCCCTTTG	CGGCTTTGCA	GCGCAGCGCC	TCCACGGACC	9300
CGTTGTGGGA	ATGCCGGCGC	TGTGCGCTGG	GCGATGTCGA	TGGAACCATC	TCGATCAACG	9360
TCGCCGSCAA	CGAGGGCGCC	AGCAGTTCCG	TCTTGCCGAT	GTGAAACGCA	CATCAGGACG	9420
CCTTTCCACC	AGCCAACTAC	GTGGGCGCCC	AACGGGTGCC	GATACATCGA	CTCGATTCCG	9480
TGGCTGCAGA	CGTTCTGCGG	CCCAACGATA	TTGCGTTCTT	GAAGATCGAC	GTTCAAAGGAT	9540
TCGAGAAGCA	GGTGATCGCG	GGTGGCGATT	CAACGGTGCA	CGACCGATGC	GTCGGCATGC	9600
AGCTCGAGCT	GTCTTTCCAG	CCGTTGTACG	AGGGTGGCAT	GCTCATCCGC	GAGGCGCTCG	9660
ATCTCGTGG	TTGCTTGGGC	TTTACGCTCT	CGGGATTGCA	ACCGGTTTTC	ACCGACCCCC	9720
GCAACGGTCG	AATGCTCGAC	GCCGATGGCA	TCTTCTTCCG	GGGCAGCGAT	TGACGCGCCG	9780
GCGCGTCAAT	CTATTTTCGAC	ATTGCGGTGA	AGACGTTTTC	CCAGAATCGA	CTGTTGTAGG	9840
CGTAGAACTC	CCGGCCCGCT	AGGTAGGCAT	GTGATATTGC	CCTTCCCCCG	AACGGGTAGC	9900
GGCGATGAAG	GTGCGCCATG	CGGCGCAGAT	CACCGAAGAC	GCGGCTTGGT	TCCCGGTGCG	9960
AGCCGACGCC	CGTGGTGTGC	AACTGCGACA	GCACACACCG	AATCGTGACC	GGCTCGCATA	10020
CCAGCGCGGC	CCGCAATATG	AATTCTTGGT	CGGCGGCGAT	CCCGAAATCA	AGGTCGTAGC	10080
CACCGATCTT	GGCCACCAGC	GATGATCCGA	AGAACGATGC	TTGATGCGGA	ACAACCTGCT	10140
TGCCGSCCAG	GAATTITGCG	AGGCTGAAAG	GTATCGGGCC	GCGCACCCGA	TCGAGCCCGA	10200
CGAGACGATC	CATCCCAGAA	CCCCACAATT	CGSACACCGG	TCCCTTGCCG	GATAGCGCCT	10260
CCACGGCCTG	GGCTACCACG	TCGGGCCCCG	AAAAACGATC	GGCGAGTGC	AAGAACCACA	10320
ACAGATCACC	CGATGCGTGC	GCGATGCCCT	GGTTTATCGC	GTGATACCGC	CCGCGCTCGG	10380
GCTCGGACTG	CCAATACGCG	AAGCCTGGTT	CACACCCGGA	CAGGTATGCC	ACCACGTGCT	10440
CGCCGCTGCC	ACCGTCGATT	ACGATGTGCT	CGATGCGTCC	CCGSTATCGT	TGCGCCCGCA	10500
CACCTTTTAC	CGTGCGCTGC	AACCCGTCGA	GGTCGTTGAA	CGAGATCGTT	ATCACCAGAA	10560
CGGTCGGAGC	AGAAGTCACC	GAGTTCCCTT	AGGTTGCTGG	CGCGGATTGT	GGATCACCGG	10620
GTCTTGATAC	CGATGAAGGT	GCCTCGAAGA	TTGCCCGCAT	AGGAACCTCC	GAGCAACGAC	10680
TCGGCGATGC	TTGGTTCCAA	GTGTTGCTAC	TCCTCCATCA	CCAGGTGCGC	GCCGACGTCT	10740
TTGATGGCCT	GAAGTAGGTG	CTCGCGTTGA	ATCCAGAAATG	ACCGGCGATT	GTCCACGAGC	10800



GCCCACTTTTG	CGGTGTCGCG	CTGGCCAACAG	GAGCGGTCGT	CGGAAAACTC	GGTAAACCAC	10860
CTACCCGGAA	GTCCCTCATG	TTCGGTGGGC	GCCGAGAGCA	TGAAC TTCAC	CGGCCCGCGC	10920
CGCCGCAGCA	ACCGATCGGT	CAATTGTCGT	GCCGTCGTGG	GCAACCGGAG	CCATTTATCG	10980
CTCCGGTTGA	TGATCAGAAA	GTGCGTCTGG	AGAATCAGCA	GCTTGTTCTGT	TACCGACGAG	11040
AGGGTTTCCA	GGTATTGCTT	CGGATTCTCC	AGGTGGTAGA	AGAGGCCCGCA	GCAGAAAGACG	11100
GTATCGAAGA	GCCCSTGGTT	GCGCATGTTG	AGGGCGTTGT	CGTGGACGAA	CCG GAGATT C	11160
GGCAGGTTGG	TCTTCGATTT	GATGTAGTTG	CAGGCCGCCA	TGTT CAGCTC	GC GAACCTCG	11220
ATCCCCAGGA	CCTGAAATCC	CATGCGCGCG	AACCCGACCG	CGTACCCGCC	TTCCAAGCAG	11280
CCGACATCGG	CCAGGCGTAG	GTGGCTCTTG	TCCCCGGGAA	AGACGGITTC	CAGAATCCCG	11340
CGCGCCGAGA	TGAACCGAGG	CGATTCTGCT	AACGTGCGCG	AGGACTCCGG	TATCGTCAA G	11400
GTTCCGTCGT	CGAGGCGAAC	GTTGTGGGCG	GTGAATTGTA	CCGCGCCGGC	CGAATGTTCC	11460
TGTGCCATCA	CTTGTTAGC	CCCTTCGGCT	GGTCCTGGGT	TGTGCGACAT	GGTCAGGCTC	11520
GACAGCCGCG	TCGGAGCCGG	GAGGGCCACA	CATCCACGAG	CCCCCTGCGG	CTCGGCGT CG	11580
CGGCGGCGAG	CTTGCGCCAC	TGGGTCTTGA	GCCGCCGCGC	GGGTGTCGCC	CCGCGGTGCT	11640
GCAGCGCCAG	CATGCGCATC	CGGGGATGGC	GCGCGATGGT	TTCTGCGAGC	GC GGCGCGCC	11700
CCTCCGGGCC	TGGAACGTTG	GCGATCTGGC	GAAGGATCCA	GTCGGCCATG	ACGGCGATGA	11760
GCTCCTCGCG	CGCGGGGTCT	CCCGGGAACA	GGTCGAGCAT	CGCGTCAAAC	GTCGCCGCAT	11820
GCCCCGGACC	CTGCGTCAAC	CAGAACTTTG	GCGGGTCCAC	CACCTGGITTG	TGCCACATGC	11880
CTTGGGCGTG	GCGGCGATAC	ACGGCCATGG	TGTCGGGCAA	CATGGCGATG	TCGCCATGCA	11940
CCGCGTGCCG	GACGTGCAGA	TACCA GTCCA	GGGGCATGAC	GTCGGCAGGA	ATGTCGTCTGT	12000
AGCGCTCGAG	GCGACG GTAC	ACGGCCGAGT	TG GTCTGGAT	GAAGTTCATC	AAGATCAACG	12060
CATCCAGGCT	CAAGTTGCCC	CGCACCCGAA	CCGGGGGGAA	CTTCGAGTCC	TTGGCATGGC	12120
CGTCTCCCA	TATCACTCGG	ACGGGATGGA	AGCACACCGT	CGTCTTGGGG	TGCCGGTCGA	12180
GG AATCGCAC	CTGTTTGCTT	AGCTTCAGCG	GATCGATCCA	G TAGTCGTCC	GCCTCGCACA	12240
ACGCGACGTA	CTCGCCGCGA	GCGGCCGACA	GGGCGCCGGT	CAGGT TCCCA	TTGAGGCCGA	12300
GGTTTTGCGT	CCTGAAGATC	GCCCGGAACA	CGTGCGGGTA	CCGCTCGGCG	TACTCACGGA	12360
TGATCGCCGG	GGTGGCATCG	GTCGACGCGT	CGTCGGCGAC	GATGATCTCC	ACCGGGAAGT	12420
CGGTTTGCTG	GTGAGAAAAG	CTGTGCAAGG	CCTGACGGGC	G TAGCCCCGC	TGTTTG TGAG	12480

TGGTCGAGAC GATGCTCACC TTGGGGCAAA GCTGGGGACT CACCGTCGGC CCTTTTCCTG 12540  
 CGCGGCCGCA AGGGTATTGC GATGGCGAAC GTGAATCGCC TGTGCCCGCC GGCCGTCGGC 12600  
 CGTCGTGGCC TGGTGGTCGG CGBACGTACG GCACACGCTG GCGAAGTATA GCGAGGGTGC 12660  
 ACTGACGTTG GGCTCGAACC GCGTGGCGCG CGGTGTGGGC GCACCGTCTC GAGTCGGTGC 12720  
 TGATTGGCTC GC 12732

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATACTCAAGC TTGCCGCAAT CGAAACCAAC CTGTTTGTGC CGCAAGAAAT TACGCCGTGG 60  
 CCCGCGCCGC ATCAAGAAAC GCCCGGCGCG GCGGCGGTGT CGTCGTATGG CATGACGGGC 120  
 ACCAATGTGC ACGCCATTGT CGAGCAGGCA CCGGTGCCAG CCCCCGAATC CGGTGCACCA 180  
 GGCACACCC CGGCCACAC CGGTATCGAC GCGCGCTGTC TGTTCGCGCT GTCGGCCAGC 240  
 TCGCAGGACG CGCTGCGGCA AACCGCCGCG GCGTGGCCG ATTGGGTCT 289

## (2) INFORMATION FOR SEQ ID NO: 3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TTGGCGGGTT GGCCACACAC CGCCCGGTGA CGGCGACGAT GCTGGGCTGG TTGCGCCCTT 60  
 GCGCCACCGC GGCTTGCAATG CTGTTGGCT GTCTTGGGAC GATCCCGAAA TAGTCCACGC 120  
 GGATCTGGTG ATTTTGCGGG CTACCCGCGA TTACCCCGCG CGGCTCGACG AGTTTTTGGC 180

0957345 113000



CAAAATGGGG GCCGCCGCGC CAGGTATCTC GCGGAAGATC CCCGGCGCTC GAGCGCTTTG 1140  
TCAGAGGCCC GTCGCGGGTC GTCGTGACGA CGGCTATCCG GCGCGTGCGG GTTTCGCGGC 1200  
GCGCCTGTG CCCGGCACCG CCGCCCGTTT GTCGGCAACG CCGCCGCGAC CCGTGAGCG 1260  
TCCAGCAGCT GCGCCTGCG 1280

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GGGCATCGGC GGAATCGGCG GTAACGCTAA CGGGGGCGCC GGTGGGAACG GCGGCACCGG 60  
CGGTGAGTGA TGGGTAGCG GCGGCGCCGG CGTCGAAGGC GCGCAGCCT TAAGCGTCGG 120  
CGACACC 127

03673476.113000